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Sequence 14523, Application US/11045024 Publication No. US20050271676A1 GENERAL INFORMATION:
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Best Local Similarity
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10, Appl
10, Appl
10, Appl
10, Appl
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822, App
126, App
832, App
69, Appl
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10517, A
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Sequence 54, Appl
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                                                                             February 22, 2006, 21:58:19; Search time 0.880829 Seconds (without alignments) 287.324 Million cell updates/sec
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1: /cgn2_6/prodata/2/pubpaa/US08 NEW FUB.pep:*

2: /cgn2_6/prodata/2/pubpaa/US06_NEW FUB.pep:*

3: /cgn2_6/prodata/2/pubpaa/US07_NEW FUB.pep:*

4: /cgn2_6/prodata/2/pubpaa/PCT_NEW FUB.pep:*

5: /cgn2_6/prodata/2/pubpaa/US07_NEW FUB.pep:*

6: /cgn2_6/prodata/2/pubpaa/US10_NEW FUB.pep:*

7: /cgn2_6/prodata/2/pubpaa/US10_NEW FUB.pep:*

8: /cgn2_6/prodata/2/pubpaa/US11_NEW FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-106-932-11

US-11-106-932-11

US-11-106-932-11

US-11-045-024-14247

US-11-045-024-14247

US-11-033-039-032

US-11-106-932-69

US-11-107-932-69

US-11-174-816-43

US-11-174-816-41

US-11-072-512-3209

US-11-174-816-11

US-11-072-14

US-11-072-14

US-11-012-762-14

US-11-012-762-14
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US-11-090-878-54
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                                                                                                                                                                                                                                117670 segs, 14887254 residues
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Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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94
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Match Length DB
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No.
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Sequence 70, Appl Sequence 3210, Appl Sequence 317, Appl Sequence 1062, Appl Sequence 1062, Appl Sequence 1056, Appl Sequence 1034, Appl Sequence 1034, Appl Sequence 1034, Appl Sequence 21, Appl Sequence 21, Appl Sequence 26, Appli Sequence 21, Appl Sequence 26, Appli Sequence 26, Appli Sequence 21, Appl Sequence 2496, Appli Sequence 2496, Appli Sequence 2496, Appl
US-11-106-932-70 US-10-46-67-9210 US-11-07-512-3879 US-10-45-372-1062 US-10-453-372-1060 US-10-453-372-1060 US-11-025-834A-13 US-10-995-561-1034 US-11-099-561-1034 US-11-099-561-1034 US-11-099-561-1034 US-11-099-661-1087 US-11-099-661-1087 US-11-099-661-1087 US-11-099-661-1087 US-11-109-661-1087 US-11-109-661-1087 US-11-100-640-6
103 103 103 204 103 100 100 100 100 100 100 100 100 100
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Colon Unders: US 08/027, 146
PRIOR FILING DATE: 1993-10-05
PRIOR FILING DATE: 1993-11-29
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastesEQ for Windows Version 4.0
SEQ ID NO 14523 OTHER INFORMATION: Standard Peptide 507.02 TYPE: PRT ORGANISM: Artificial Sequence

Score 94; DB 7; Length 24; Pred. No. 1.6e-09;

100.0%;

us-10-000-439-13.rapbn

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Sequence 11, Application US/11106932
Publication No. US20050260697A1
GENERAL INFORMATION:
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Publication No. US2006002947A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: HUMPHREWS.

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/11/033,039

CURRENT PILING DATE: 2005-01-11

FRIOR FILING DATE: 2005-01-11

FRIOR FILING DATE: 2002-09-17

FRIOR FILING DATE: 2002-09-17

FRIOR FILING DATE: 1999-09-14

FRIOR FILING DATE: 1999-09-14
                                                                                                                                                                                                  US-11-000-878-54

Sequence 54, Application US/11090878

Sequence 54, Application US/11090878

Sequence 54, Application O. US20050244911A1

GENERAL INFORMATION:

APPLICANT: Saus, Juan

TTYLE OF INVENTION: Methods and Reagents for Identifying Compounds for TYLE OF INVENTION: Treating Autoimmune Disorders

FILE REFERENCE: 98-723-C3

CURRENT RPLICATION UNMERR: US/11/090,878

CURRENT FILING DATE: 2005-03-25

NUMBER OF SEQ ID NOS: 84

SOFTWARE: Patentin Ver. 2.0
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          0; Indels
       Mismatches
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                                                       1 ENPVOHERMIVTPRIP 17
                                                                                                     6 ENPVVHFFKNIVTPRTP 22
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ORGANISM: Artificial Sequence
       17; Conservative
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US-11-033-039-824
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LENGTH: 197
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RESULT 4 US-11-106-932-11

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APPLICANT: WANG, KA-WANG KEVIN
APPLICANT: WANG, KA-WANG KEVIN
APPLICANT: HAYES, RONALD
APPLICANT: LIU, MING CHEN
APPLICANT: LIU, MING CHEN
APPLICANT: OLI, MONTO
TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
FILE REPRESENCE: 5863-549-11
CURRENT APPLICATION NUMBER: US/11/106,932
CURRENT PILING DATE: 2005-04-15
NUMBER OF SEQ ID NOS: 147
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APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/11/150, 755
CURRENT FILING DATE: 2005-06-10
PRIOR FILING DATE: 2002-12-09
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 1
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OTHER INFORMATION: Immunodominant peptide of MBP, recognized by
OTHER INFORMATION: HLA-DR2 haplotype
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100.0%; Pred. No. 8.7e-08;
cive 0; Mismatches 0; Indels
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94.4%; Pred. No. 1.1e-07;
tive 0; Mismatches 0;
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SEQ ID NO 11
LENGTH: 30
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Best Local Similarity 94.4
Matches 17; Conservative
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Matches 15; Conservative
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ORGANISM: Homo sapiens
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US-11-150-755-69
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US-11-150-755-1
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Gaps

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Sequence 126, Application US/10893584

Publication No. US20050272048A1

GENERAL INFORMATION:

APPLICANT: Borgford, Thor

APPLICANT: Braun, Curtis

APPLICANT: Braun, Curtis

APPLICANT: Braun, Curtis

APPLICANT: Braun, Curtis

TITLE OF INVENTION: Viral or Parasitic Infections

TITLE OF INVENTION: Viral or Parasitic Infections

TITLE REFERENCE: 10447-025

FILLE REFERENCE: 10447-025

CURRENT APPLICATION NUMBER: US 09/551,151

PRIOR FILLING DATE: 2004-01-19

PRIOR FILLING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 2000-10-44

PRIOR FILING DATE: 2000-10-44

PRIOR FILING DATE: 2000-10-44

SEQ ID NOS: 274

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 126
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; OTHER INFORMATION: Mutant preproricin linker region for calpain, pAP-296
US-10-893-584-126
                                                                                                                                                                                                                                                                                                                                          | Sequence 822, Application US/11033039 |
| Sequence 822, Application US/11033039 |
| Publication No. US2006002947A1 |
| GENERAL INFORMATION: |
| APPLICANT: HUMPHREYS, ROBERT |
| APPLICANT: HUMPHREYS, ROBERT |
| APPLICANT: KU, MINZHEN EN FILES / ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES |
| TITLE OF INVENTION: LI-EXF/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES |
| FILE REFERENCE: REH-2017US01 |
| CURRENT APPLICATION NUMBER: 10/245,871 |
| PRIOR FILING DATE: 2002-09-17 |
| PRIOR FILING DATE: 2002-09-17 |
| PRIOR FILING DATE: 1999-09-14 |
| PRIOR FILING DATE: 1999-09-14 |
| RIOR FILING DATE: 1999-09-14 |
| NUMBER OF SEQ ID NOS: 1452 |
| SEQ ID NO 822 |
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        Mismatches
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ORGANISM: Artificial Sequence
                                                                                                                                            1 WHFFKNIVTPRTP 14
                                                                                  4 WHFFKNIVTPRTP 17
        14; Conservative
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; ORGANISM: Homo sapiens
US-11-033-039-822
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Best Local Similarity
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US-10-893-584-126
                                                                                                                                                                                                                                                                                                                     US-11-033-039-822
        Matches
                                                                                                                                                                                                                                                                                RESULT 8
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APPLICANT: Siette, Alessandro
APPLICANT: Siette, Alessandro
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Esteban
APPLICANT: Esteban
APPLICANT: Esteban
APPLICANT: Rubo, Ralph
APPLICANT: Rubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Bpimmun Inc.
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE OF INVENTION: Virus-1 Using Deptide and Nucleic Acid Compositions
FILE OF INVENTION: Virus-1 Using Deptide and Nucleic Acid Compositions
FILE OF INVENTION NUMBER: US 09/412,863
FRIOR APPLICATION NUMBER: US 08/027,146
FRIOR APPLICATION NUMBER: US 08/103,396
FRIOR PILING DATE: 1993-03-05
FRIOR PILING DATE: 1993-11-29
FRIOR PILING DATE: 1993-11-29
FRIOR APPLICATION NUMBER: US 08/159,339
FRIOR PILING DATE: 1994-03-04
FRIOR FILING DATE: 1994-03-04
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TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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COTHER INFORMATION: The peptide was designed and synthesized.

US-11-150-755-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 84.0%; Score 79; DB 7; Length 15; Best Local Similarity 93.3%; Pred. No. 2.7e-07; Matches 14; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 16; 9e-07;
                                 FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/11/150,755
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US/10/056,583
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.9%; Score 76; 100.0%; Pred. No.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14247
LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14247, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ENPVVHFFKNIVTPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ENPVOHYFKNIVTPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sette, Alessandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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LENGTH: 15
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US-11-14-816-43
is Sequence 43, Application US/11174816
publication No. US2006009441A1
idention No. US2006009441A1
idention No. US2006009441A1
idention No. US2006009441A1
idention No. USELING, MARTIN
idention No. USELING, MARTIN
idention Indomann, LOTHAR
ittle Net INTENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS
ittle REFERENCE: 22645
icurrent APPLICATION NUMBER: US/11/174,816
icurrent APPLICATION NUMBER: EP 04103261.6
iprior APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
41.5%; Score 39; DB 7; Length 337;
Best Local Similarity 26.7%; Pred. No. 33;
Matches 8; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 7; Length 574; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR PELLING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
              Sequence 3209, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROVIKI
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533 ESPRIHPTRIPKTPRTP 549
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3209
LENGTH: 574
                                                                                                                                                                                                                                                                                                                                                                                               NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                    OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-072-512-3209
                                                                                                                                                                                                                                                         APPLICANT
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| Sequence 80.2, Application US/11033039
| Publication No. US20060002947A1
| GENERAL INFORMATION:
| APPLICANT: HUMPHREXS, ROBERT
| APPLICANT: W. MINZHEN
| TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| FILE REFERENCE: REH-2017US01
| CURRENT PAPLICATION NUMBER: 10/245,871
| PRIOR PLILING DATE: 2005-00-17
| PRIOR PLLING DATE: 2002-09-17
| PRIOR PLLING DATE: 2002-07-17
| PRIOR PLLING DATE: 2002-07-17
| PRIOR PLLING DATE: 1002-07-17
| PRIOR PLLING DATE: 1002-07-17
| PRIOR PLLING DATE: 1995-09-14
| NUMBER OF SEQ ID NOS: 1452
| SEQ ID NO 832
| LENGTH: 9
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  Indels
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0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
11; Conservative
                                                        7 FFKNIVTPRTP 17
                                                                                               1 FFKNIVTPRTP 11
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US-11-106-932-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens US-11-033-039-832
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US-11-033-039-832
  Matches
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RESULT 12

2 NPVVHFF-----KNIVTPRTP 17

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                                                                              RESULT 14
US-11-174-819-11

i Sequence 11. Application US/11174819

i Publication No. US2006000880A1

i GENERAL INFORMATION:
APPLICANT: BEBLING, MARTUN
APPLICANT: HOENER, MARTUN
APPLICANT: LINDEMANN, LOTHAR
ITILE OF INVENTION: MOUSE TRACE AMINE ASSOCIATED RECEPTORS AND
ITILE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 22646
CURRENT APPLICATION NUMBER: US/11/174,819
CURRENT APPLICATION NUMBER: EP 04103262.4

PRIOR PILING DATE: 2004-07-08
NUMBER OF SEQ ID NOS: 136

SOFTWARE: Patentin version 3.3

SEQ ID NO 11

LEMETH: 337

LEMETH: 337
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| Sequence 40, Application US/11075046
| Publication No. US20050268353A1
| Publication No. US2005026835A1
| GENERAL INFORMATION:
| APPLICANT: P. D. CHRISTIAN, K. H. J. GORDON and
| APPLICANT: T. N. HANZLIK
| TITLE OF INVENTION: INSECT VIRUSES AND THEIR USES IN
| TITLE OF INVENTION: PROTECTING PLANTS
| TITLE OF SEQUENCES: 53
| CORRESPONDENCE ADDRESS: ADDRESSE: DORSEY & WHITHEY LLP
| STREET: FOUR EMBARCADERO CENTER, SUITE 3400
| CITY: SAN FRANCISCO STATE: CALIFORNIA
| COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPY disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/075,046
FILING DATE: 07-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/677,653
FILING DATE: 03-0ct-2000
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD F. TRECARTIN
REFIRENCE/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-4/RFT/NBC
301 NPIIYVFSYRWFRKALKLLLSREIFSPRTP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NPVVHFF-----KNIVTPRTP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
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Query Match
Best Local Similarity
US-10-104-973-3
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   LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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Sequence 2, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
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30, Appl
35, Appl
49, Appl
26, Appl
1, Appl
1, Appli
1, Appli
1, Appli
1, Appli
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Sequence 1220, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Appli
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                                                                                                     February 22, 2006, 21:57:24; Search time 8.69085 Seconds (without alignments) 817.308 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Sequence 6, Sequence 12, Sequence 13, Sequence 14, Sequence 28, Sequence 28, Sequence 36, Sequence 36, Sequence 28, Sequence 36, Sequence 28, Sequence 28, Sequence 26, Sequenc
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Sequence
Sequence
Sequence
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Sequence
Sequence
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                GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-104-973-3

US-10-000-439-13

US-10-232-892A-2

US-10-482-044-5

US-10-70-712-6

US-09-740-001-2

US-09-76-872-1

US-09-76-872-1

US-09-76-872-1

US-09-76-872-1

US-09-76-872-1

US-09-76-872-1

US-09-76-872-1

US-09-859-012-35

US-09-859-012-35

US-09-859-012-35

US-09-859-012-35

US-09-859-012-35

US-09-859-012-36

US-09-859-012-36

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US-10-9859-012-36

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US-10-149-138-4219

US-10-149-138-4219
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US-10-654-601-2501
US-11-051-411-1220
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US-10-149-138-4219
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                      US-10-000-439-13
94
1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score:
                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                          Seguence:
                                                                                                                                                                                                                                                                                    Searched:
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Sequence 1, Appli
Sequence 1, Appli
Sequence 115, Appl
Sequence 339675,
Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 2, Appli
Sequence 12, Appli
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APPLICANT: Gaur, Amitabh
APPLICANT: Gaur, Paul J.
APPLICANT: Conlon, Paul J.
APPLICANT: Staehlin, Theophil
APPLICANT: Staehlin, Theophil
APPLICANT: Crowe, Paul D.
TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
FILE REFERENCE: 690068.405C4
CURRENT APPLICATION NUMBER: US/10/104,973
CURRENT APPLICATION NUMBER: US/10/104,973
CURRENT FILING DATE: 2002-03-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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US-10-000-439-13

i Sequence 13, Application US/10000439

i Publication No. US20030064063A1

i GENERAL INFORMATION:

i APPLICANT: Saxon, Andrew

i TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR

ITILE OF INVENTION: TREATMENT OF IMMUNE DISEASES

FILE REFERENCE: UCG67.004A

CURRENT FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: US 09/847,208

PRIOR PELLING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FASELSEQ for Windows Version 4.0
  US-09-813-183-1
US-09-813-463A-1
US-0-813-463A-1
US-10-492-794-115
US-10-425-115-339675
US-10-475-110-32
US-10-126-834B-1
US-10-199-995-3
US-10-199-995-3
US-10-199-995-3
US-09-989-476-2
US-10-104-973-2
US-10-104-973-2
US-11-004-439-12
                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10104973 Publication No. US20020176866A1 GENERAL INFORMATION:
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US-10-402-04-5.

Subjication US/10482044

Publication No. US20040235713A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Glycopetides, their preparation and use in the diagnosis or TITLE OF INVENTION: therapeutic treatment of multiple sclerosis

TITLE REFERENCE: 2744 FTWO

FULLE REFERENCE: 2734 FTWO

CURRENT APPLICATION NUMBER: US/10/482,044

CURRENT APPLICATION NUMBER: PCT/FP 02/06767

PRIOR PILING DATE: 2003-06-19

PRIOR PILING DATE: 2002-06-19

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CARBOHYD
LOCATION: (2)..(2)
OTHER INFORMATION: the carbohydrate is beta-D-glucopyranosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-770-712-6
; Sequence 6, Application US/10770712
; Publication No. US20050170333A1
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFERENCE: IMSC12.008A
; CURRENT APPLICATION NUMBER: US/10/770,712
; UURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 17
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100.0%; Score 94; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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          100.0%; Score 94; DB 4; Length 17; 100.0%; Pred. No. 5.3e-08; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: glycopeptide
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ORGANISM: Artificial Sequence
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       Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity 100.0
watches 17; Conservative
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US-10-482-044-5
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LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Score 94; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 5.3e-08;

Matches 17; Conservative 0; Mismatches 0; Indels
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Publication No. US20040043431A1
ABDLICATION:
APPLICANT: Vojdani, Aristo
TITLE OF INVENTION: DIAGNOSIS OF MULTIPLE SCLEROSIS AND
TITLE OF INVENTION: OTHER DEMYELINATING DISEASES
FILE REFERENCE: INSMS.001A
CURRENT APPLICATION NUMBER: US/10/233,892A
CURRENT FILING DATE: 2002-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-362-264-1
Sequence 1, Application US/10362264
SUBLICATION NO. US20030191063A1
GENERAL INFORMATION:
APPLICANT: Wraith, David
APPLICANT: Maza, Graziella
APPLICANT: Ponsford, Mary
APPLICANT: Ponsford, Mary
APPLICANT: The University of Bristol
APPLICANT: The University of Bristol
TITLE OF INVENTION: PEPTIDE SELECTION METHOD
FILE REFERENCE: 1433.004US1
CURRENT APPLICATION NUMBER: US/10/362,264
CURRENT APPLICATION NUMBER: 027/GB01/03702
PRIOR APPLICATION NUMBER: 027/GB01/03702
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2001-08-17
SPRIOR FILING DATE: 2001-08-17
SPRIOR FILING DATE: 2001-08-17
SPRIOR FILING DATE: 2001-08-17
SPRIOR FILING DATE: 2001-08-11
SOFTWARE: PATENTIN NUMBER: 0114547.3
NUMBER OF SEQ ID NOS: 11
SEQ ID NO
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                       TYPE: PRT ORGANISM: Homo sapiens US-10-000-439-13
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SEQ ID NO 13
LENGTH: 17
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PRIOR FILING DATE: 1999-03-09
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Matches 17; Conserv
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Sequence 1, Application US/09768872
Patent No. US20020055466A1
GENERAL INPORMATION:
APPLICANT: Aharoni, Ruth
APPLICANT: Feitelbaum, Dvora
APPLICANT: Fridkis-Harelli, Masha
APPLICANT: Browninger, Jack
TITLE OF INVENTION: and Related Copolymers and Peptides
FILE REFERENCE: 162/493762
CURRENT APPLICATION NUMBER: US/09/768,872
CURRENT FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: US 60/102,960
PRIOR FILING DATE: 1998-10-02
PRIOR FILING DATE: 1998-10-02
PRIOR FILING DATE: 1998-11-0-02
PRIOR PLING DATE: 1998-11-12
PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: US 60/108,184
PRIOR FILING DATE: US 60/123,675
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SEQUENCE 2, APPLICATION NO. US20020039582A1

GENERAL INFORMATION:

APPLICANT: RASTETTER, WILLIAM H.

APPLICANT: BLACK, MABELIA

TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES

CURRENT APPLICATION NUMBER: US/09/740,003

CURRENT APPLICATION NUMBER: US/09/740,003

FILE REFERENCE: 37003/27380

FILE REFERENCE: 1998-02-17

FRIOR PILING DATE: 1998-02-17

FRIOR PELING DATE: 1998-02-07

FRIOR PELING DATE: 1994-02-07

FRIOR PELING DATE: 1994-02-07

FRIOR PELING DATE: 1994-02-07

FRIOR FILING DATE: 1997-08-29

FRIOR FILING DATE: 1997-08-29

FRIOR FILING DATE: 1991-07-25

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 2

LENGTH: 19
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1 ENPVOHEFKNIVTPRTP 17
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US-09-768-872-1
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ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP STREET: 130 Water Street
                                                                                                                                                                                                                    Query Match
100.0%; Score 94; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                               FEATURE:

COTHER INFORMATION: synthetic peptide (MBP residues 84-102)
US-09-768-872-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acevedo, Jorge
Burkhardt, Martin
Jiao, Jin-an
Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 48002-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/766,378A
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-766-378A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/960,190 FILING DATE: 29-OCT-1997
NUMBER OF SEQ ID NOS: 3
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 1
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Application US/09766378A Patent No. US20020091079A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: usa
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rhode, Peter R.
                                                                                                                                                                                                                                                                                                              1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                     ENPVVHFFKNIVTPRTP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
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Gape
                                                                                                                                                Gaps
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: peptide US-10-743-398-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 94; DB 3; Length 20; 100.0%; Pred. No. 6.4e-08; ive 0; Mismatches 0; Indels
                                                                                                Length 19;
                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYRE: DBRACHE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,378A
FILING DATE: 19-Jan-2001
CLASSIFICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acevedo, Jorge
Burkhardt, Martin
Jiao, Jin-an
Wong, Hing Couplexes AND
TITLE OF INVENTION: SOLUBLE WHC COMPLEXES AND
METHODS OF USE THEREOF
                                                                                                100.0%; Score 94; DB 4;
100.0%; Pred. No. 6e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COTIESS, PETER F
REGISTRATION NUMBER: 33,860
REGISTRATION NUMBER: 48002-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQ ID NO: 28: US-09-766-378A-28
                                                                                                                                                                                                                                                                                                                                   US-09-766-378A-28
; Sequence 28, Application US/09766378A
; Patent No. US20020091079A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: usa
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ENPVOHEFKNIVTPRIP 17
                                                                                                                                                                                              1 ENPVWHEFKNIVTPRTP 17
                                                                                                                                                                                                                                          2 ENPVOHEFKNIVTPRTP 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                       RESULT 10
US-10-239-313A-143
is Sequence 143, Application US/10239313A
is Sequence 143, Application US/10239313A
is Sequence 143, Application No. US20030175285A1
is Dublication No. US20030175285A1
is Deblication No. US20030175285A1
is APPLICANT: KUINGUR. HAMOUR, Christine
is APPLICANT: CORNALW. Nathalie
is APPLICANT: GORECLE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
it TILE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
it TILE OF INVENTION: NO. PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
it TILE OF INVENTION NUMBER: US/10/239,313A
icurrent APPLICATION NUMBER: PCT 01/70712
ip PRIOR PILING DATE: 2000-03-23
ip PRIOR PILING DATE: 2000-03-23
ip PRIOR FILING DATE: 2001-03-22
invender Of Seq ID NOS: 697
is SOFTWARE: PatentIn Ver. 2.1
is LENGTH .10
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APPLICANT: RAYCHAUDHURI, SYAMAL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: BLACK, AMBLIA
TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
FILE REFERENCE: 37003/307430
CURRENT APPLICATION WUMBER: US/10/743,398
CURRENT PILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: 09/740,003
PRIOR PILING DATE: 1998-02-17
PRIOR PILING DATE: 1998-02-17
PRIOR PILING DATE: 1998-02-17
PRIOR PILING DATE: 1999-02-17
PRIOR PILING DATE: 1999-02-17
PRIOR PILING DATE: 1999-06-07
PRIOR PILING DATE: 1999-06-07
PRIOR PILING DATE: 1999-06-07
PRIOR PILING DATE: 1999-08-29
PRIOR PILING DATE: 1991-08-29
PRIOR PILING DATE: 1991-07-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VOY: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 94; DB 4; Length 19; Best Local Similarity 100.0%; Pred. No. 6e-08; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10743398 Publication No. US20040197331A1 GENERAL INFORMATION:
                                      ENPVWHFFKNIVTPRTP 17
                                                                   1 ENPVWHERKNIVTPRIP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ENPVVHFFKNIVTPRTP 17
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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APPLICANT: WITTMAN, VAUGHAN
APPLICANT: WITTMAN, VAUGHAN
APPLICANT: WITTMAN, VAUGHAN
APPLICANT: WITTMAN, UANTIN
APPLICANT: CARD, KIMBERLYN F.
APPLICANT: TAL, KONY
APPLICANT: TAL, KONY
APPLICANT: TAL, RONY
APPLICANT: WONG, HING C.
TITLE OF INVENTION: MODILATION OF T CELL RECEPTOR INTERACTIONS
FILE REFERENCE: 49444 (71756)
FILE REFERENCE: 49444 (71756)
CURRENT APPLICATION NUMBER: US/09/859,012
CURRENT FILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 35
LENGTH: 20
TYPE: FRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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100.0%; Score 94; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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                 Sequence 30, Application US/09836433
Publication No. US20030049797A1
GENERAL INFORMATION:
APPLICANT: Yoshikazu
APPLICANT: Udaka, Shigazo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REPERENCE: No. US20030049797A1 Assigned
CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/09859012
Publication No. US20040253632A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ENPVOHEFKNIVIPRTP 19
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                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Bynthetic construct
US-09-836-433-30
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Matches 17; Conservative
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US-09-859-012-49
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US-09-859-012-35
US-09-836-433-30
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                                                                                                                                                                                                                                                                            SEQ ID NO 30
LENGTH: 20
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| APPLICANT: WEIDANZ, JON A. | APPLICANT: WEIDANZ, JON A. | APPLICANT: BURKHARDY, WARTIN | APPLICANT: CARD, KIMBERLYN F. | APPLICANT: CARD, KIMBERLYN F. | APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: WONG, HING C. | TITLE OF INVENTION: WODULATION OF T CELL RECEPTOR INTERACTIONS | TITLE OF INVENTION: WODULATION NUMBER: 05/206,920 | TITLE OF INVENT APPLICATION NUMBER: 06/206,920 | PRIOR PAPLICATION NUMBER: 06/206,920 | PRIOR FILING DATE: 2000-05-25 | NUMBER OF SEQ ID NOS: 49 | SEQ ID NOS: 40 |
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TYPE: PRT
ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity
Matches 17; Conserv
RESULT 1
US-09-137-759-3
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Sequence 18, Appli
Sequence 2, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
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556.619 Million cell updates/sec
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                                                       February 22, 2006, 21:37:34 ; Search time 2.52504 Seconds
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Sequence 32,
Sequence 2, A
Sequence 15,
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Sequence 28,
Sequence 1, Al
Sequence 46,
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Sequence 46,
                                                                                                                                                                                                                                                                                                                                                                 Description
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Sequence
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        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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/cgm2_6/prodata/1/iaa/PCTUS_COMB.pep:*
/cgm2_6/prodata/1/iaa/RE_COMB.pep:*
/cgm2_6/prodata/1/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-475-399A-46
US-09-239-043D-2501
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US-08-468-5408-18

US-08-468-5408-9

US-08-468-5408-17

US-08-468-5408-17

US-08-297-395-1

US-08-297-395-1

US-08-297-395-1

US-08-297-395-1

US-08-297-395-1

US-08-661-396-3

US-08-640-344-3

US-08-640-344-5

US-08-640-344-7
                                                                                                                                                             Fotal number of hits satisfying chosen parameters:
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PCT-US93-07545-46
                                                                                                                                                572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                      US-10-000-439-13
94
1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                         Issued Patents AA:*
                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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                                       OM protein
                                                                                                        Sequence:
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28 94 100.0 40 2 US-08-297-395-2 Sequence 2, Appli 2 94 100.0 168 6 5194425-4 Sequence 1, Appli 31 94 100.0 170 1 US-08-227-372-1 Sequence 1, Appli 32 94 100.0 170 1 US-08-327-357A-1 Sequence 1, Appli 33 94 100.0 170 2 US-08-470-397-1 Sequence 1, Appli 34 94 100.0 170 2 US-08-470-397-1 Sequence 1, Appli 34 94 100.0 170 2 US-08-62-361-3 Sequence 1, Appli 36 94 100.0 170 2 US-08-075-263-1 Sequence 1, Appli 37 94 100.0 170 2 US-08-075-263-1 Sequence 1, Appli 39 94 100.0 170 2 US-08-075-263-1 Sequence 1, Appli 39 94 100.0 170 2 US-08-08-1 Sequence 2, Appli 41 94 100.0 171 2 US-08-137-759-2 Sequence 2, Appli 42 94 100.0 171 2 US-08-313-759-2 Sequence 2, Appli 42 94 100.0 171 2 US-08-313-759-2 Sequence 2, Appli 44 94 100.0 171 2 US-09-378-244-2 Sequence 2, Appli 59 100.0 171 2 US-09-378-244-2 Sequence 2, Appli 50 171 2
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ALIGNMENTS

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US-09-137-159.

US-09-137-159.

US-09-137-159.

Sequence 3, Application US/09137759

Sequence 3, Application US/09137759

Sequence 3, Application US/09137759

Sequence 3, Application US/09137759

SPECIAL NEWEXPRONE SEARCH THEOPHIL 3.

APPLICANT: Conion, Reall J. APPLICANT: Crowe, Paul D. TITLE OF INVEXTION: EPETIDE ANALOGS OF HUWAN WYELIN BASIC PROTEIN TITLE OF INVEXTION: WIRESER: US/09/137,759

CURRENT FILING DATE: 1988-08-20

CURRENT FILING DATE: 1988-08-20

SOCTWARE: PRECHAIN OF 2.0

SOCTWARE: PRECHAIN OF 2.0

SOCTWARE: PRECHAIN OF 2.0

SOCTWARE: PRECHAIN OF 2.0

SOCTWARE: PROPARYION: Synthesis

CONTER INFORMATION: Synthesis

CONTER INFORMATION: Synthesis

US-09-137-759-3

SAGUENCE 3. Application US/09378244

SAGUENCE 3. APPLICANT: Gaut. Amitabh

APPLICANT: Conion, Reall J. APPLICANT: Crowe, Paul D. STATES SOUGH 406CC ANALOGS OF HUWAN WYELING BASIC PROTEIN

TITLE OF INVEXTION WIRBER: US/09/178,244

CURRENT FILING DATE: 1999-08-19
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RESULT 5
US-08-468-540B-9
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US-08-468-540B-18

Sequence 18, Application US/08468540B

Patent No. 5858890

GENERAL INFORMATION:

APPLICANT: Weiner, Howard

APPLICANT: Hafler, David

APPLICANT: Al-Sabagh, Ained

TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION

TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby P.C.

STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                               ) OTHER INFORMATION: Description of Artificial Sequence: Solid Phase; OTHER INFORMATION: Synthesis
US-09-378-244-3
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                                                                                                                                                                                                                                       Length 17;
                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                    Query Match 100.0%; Score 94; DB 2; L
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                          1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                    1 ENPVYHFFKNIVTPRTP 17
                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: No. 5858980e
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NY
COUNTRY: US.
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-468-540B-18
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1 ENPVVHFFKNIVTPRTP 17

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us-10-000-439-13.rai

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Sequence 24, Application US/08468540B

Patent No. S858980

GENERAL INFORMATION:
APPLICANT: Weiner, Howard
APPLICANT: Miller, Ariel
APPLICANT: Miller, Aniel
APPLICANT: Alsabagh, Ahmad
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 94; DB 1; Length 19; 100.0%; Pred. No. 8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 94; DB 1; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARR: PERSESSO for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/468,540B FILING DATE: 06-JUN-1995 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATTONNEY/AGENT INFORMATION:
                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ENPVVHFFKNIVTPRTP 18
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: No. 5858980e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 5858980e
                                                                                                                                                                             INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
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amino acid
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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; MOLECULE TYPE:
US-08-468-540B-24
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US-08-468-540B-24
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Fatent No. 588890
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weiner, Howard
APPLICANT: Miller, Arial
APPLICANT: Miller, Ari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 8e-09;
; Mismatches 0; Indels
                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM; DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN-1995
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Serh u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: DISACLET
COMPUTER: IBM COmpatible
COPERATING SYSTEM: DOS
SOFTWARE: FASESE for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: OS-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 94; DE
Best Local Similarity 100.0%; Pred. No. 8e-
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ENPVVHFFKNIVTPRTP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ENPVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: No. 5858980e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                            ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-468-540B-17
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COUNTRY:
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APPLICANT: Acevedo, Jorge
APPLICANT: Burkhardt, Martin
APPLICANT: Uso, Jin-an
APPLICANT: Uso, Jin-an
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SECUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                         APPLICATION NUMBER: US 07/919,787
FILING DATE: 24-JUL-1992
APPLICATION NUMBER: US 07/735,069
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: TESTING DATE: 25-JUL-1991
ATTORNEY/AGENT NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-149
TELECOMMUNICATION INFORMATION:
TELEPRAX: (703) 836-6620
TELECOMMUNICATION NO. 2:
SEQUERAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 94; DB 2; Best Local Similarity 100.0%; Pred. No. 8e-09; Matches 17; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-OCT-1997
                                                             APPLICATION NUMBER: 08/476,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-960-190A-32
; Sequence 32, Application US/08960190A
; Patent No. 6232445
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33,860
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ENPVVHFFKNIVTPRTP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ENPVWHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/ABGNT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,88
                                        PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: us
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-024-220-2
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STATE: Virginia
COUNTRY: United States
ZIP: 2231-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,220
FILING DATE: 17-Feb-1998
CLASSIPICATION: «Unknown»
24-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09024220
Patent No. 6197311
GENERAL INFORMATION:
APPLICANT: RAXCHAUDHURI, Syamal
RASTETTER, William H.
BLACK, Amelia
TITLE OF INVENTION INDUCTION OF CYTOTOXIC T-LYMPHOCYTE
RESPONSES
                                                                                                                                                                                                                                     Sequence 1. Application US/08297395A

Sequence 1. Application US/08297395A

GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
APPLICANT: Bavid A. Hafler
TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
TITLE OF INVENTION: PEPTIDES OF WYELIN BASIC PROTEIN
FILE REFERENCE: 1010/05723US3
CURRENT FILING DATE: 1994-08-11
EARLIER APPLICATION NUMBER: 08/059,189
EARLIER PEPLICATION NUMBER: 07/502,559
EARLIER PEPLICATION NUMBER: 07/502,559
EARLIER FILING DATE: 1990-03-30
EARLIER PELICATION NUMBER: PCT/US88/02139
EARLIER PELICATION NUMBER: PCT/US88/02139
EARLIER APPLICATION NUMBER: PCT/US88/02139
EARLIER PELING DATE: 1988-06-24

MUMBER OF SEQ ID NOS: 84

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FABSEC FOR WINDOWS 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 94; DB 2; Length 19;
100.0%; Pred. No. 8e-09;
tive 0; Mismatches 0; Indels
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
Pred. No. 8e-09;
Best Local Similarity 100.0%; Pred. No. be-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ENPVVHFFKNIVTPRTP 18
                                                                                                                 2 ENPVVHFFKNIVTPRTP 18
                                                                                     1 ENPVVHFFKNIVTPRTP 17
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US-08-297-395-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-09-024-220-2
                                                                                                                                                                                                                         US-08-297-395-1
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APPLICANT: EVELINE BERAUD
APPLICANT: EVELINE BERAUD
APPLICANT: IRINA MARIANOVSKY
APPLICANT: IRINA MARIANOVSKY
TITLE OF INVENTION: ESEUDOWONAS EXOTOXIN-MYELIN BASIC PROTEIN CHIMERIC
FILE REFERENCE: LOREBERBOUM=1
CURRENT APPLICATION NUMBER: US/09/077,028A
CURRENT FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: IL116559
PRIOR PILING DATE: 1995-11-17
PRIOR APPLICATION NUMBER: PCT/IL96/00151
PRIOR PILING DATE: 1995-11-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09740003
Fatent No. 6733763
Fatent No. 6733763
GENERAL INFORMATION:
APPLICANT: RAYCHAUDHURI, SYAMAL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: BLACK, AMELIA
ITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
FILE REFERENCE: 37003/275802
CURRENT APPLICATION NUMBER: US/09/740,003
CURRENT FILING DATE: 12090-12-20
PRIOR PILING DATE: 12958-02-17
PRIOR PILING DATE: 1998-02-17
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1997-08-29
PRIOR PILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/919,787
PRIOR PILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/919,787
PRIOR PILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/919,787
PRIOR PILING DATE: 1991-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ): OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide
US-09-740-003-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 94; DB 2; Length 19; 100.0%; Pred. No. 8e-09; cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 8e-09;
iive 0; Mismatches 0; Indels
                                       Sequence 15, Application US/09077028A
Patent No. 6531133
GENERAL INFORMATION:
APPLICANT: HAYA LORBERBOUM-GALSKI
APPLICANT: IDA STEINBERGER
APPLICANT: RIA MARIANOVSKY
APPLICANT: SHAI YARKONI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ENPVVHFFKNIVTPRTP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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Query Match

Best Local Similarity 100.0%; Pred. No. 8e-09;

Matches 17; Conservative 0; Mismatches 0; Indels
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Pred. No. 8e-09;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CALLICOTIA
COUNTRY: U.S.A.
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: ISM PS/2 Model 50Z or 55SX
COMPUTER: ISM PS/2 Model 50Z or 55SX
COMPUTER: WordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,728
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/735,069
FILING DATE: 25-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Watchurg, Richard 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SYAWAL RAYCHAUDHURI
APPLICANT: WILLIAM H RASTETTER
TITLE OF INVENTION: T-LYMPHOCYTE RESPONSES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08449728
Patent No. 6270769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRCE/DOCKET NUMBER: 194/:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                   US-08-960-190A-32
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TOPOLOGY:
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Patent No. 5824315

GENERAL INFORMATION:
APPLICANT: NUKKU, PRABHA

APPLICANT: NUKKU, PRABHA

TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC

TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

STREET: TOWNSEND & TOWNSEND & TOWNSEND
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                           US-08-640-344-1

| Sequence 1, Application US/08640344
| Sequence 1, Application US/08640344
| Patent No. 5824315
| GENERAL INFORMATION:
| APPLICANT: NUKU, PRABHA
| APPLICANT: DESHPANDE, SHRIKANT
| TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
| TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
| NUMBER OF SEQUENCES: 18
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
| ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 94; DB 1; Length 20; 100.0%; Pred. No. 8.5e-09; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,344
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP STREET: TWO EMBARCADERO CENTER, 8TH FLOOR CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INPORMATION:
NAME: STORELLA ESQ., JOHN R.
REFERANTON NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 14058-004800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
NFORMATION FOR SEQ ID NO: 1:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-APR-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENPVVHFFKNIVTPRTP 19
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ENPVVHFFKNIVTPRTP 17
                                        2 ENPVVHFFKNIVTPRTP 18
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Best Local Similarity 100.
Matches 17; Conservative
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MOLECULE TYPE: peptide
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COUNTAR: U.S.A.

ZIP: 94111-3834

COMPUTER READ-BILE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PETENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/640,344
FILING DATE: 30-APR-1996
CLASSIPICATION NUMBER: 1996
CLASSIPICATION NUMBER: 25 944
REGISTRATION NUMBER: 32 944
REFERENCE/DOCKET NUMBER: 14058-004800
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATIOS:
TELECOMMUNICATION INFORMATIOS:
TELEGOMUNICATION INFORMATIOS:
TELEGOMUNICATION INFORMATIOS:
TELEGOMUNICATION INFORMATIOS:
TELEGOMUNICATION POR SEC 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: maino acids
TYPE: peptide
SEQUENCE CHARACTERISTICS:
LENGTH: 100.0%; Pred. NO: 8.5e-09;
MACCHIE TYPE: peptide

SERVUHPFKNIVTPRTP 19

AUS-08-640-344-3

RENEVUHPFKNIVTPRTP 19
SERVUHPFKNIVTPRTP 19
SERVUHPFKNIVTPRTP 19
SEARCH completed: February 22, 2006, 21:39:50
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalais; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          050501 RAT PRELIMINARY;
050501;
13-SEP-2005 (TrEMBLrel. 31, La
13-SEP-2005 (TrEMBLrel. 31, La
13-SEP-2005 (TrEMBLrel. 31, La
Myelin basic protein.
Name=Mbp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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DD T 25-5

DT 25-5

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cavia porce
oryctolagus
bos taurus
pan troglod
sus scrofa
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sus scrofa
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mus musculu
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equus cabal
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mus musculu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xenopus lae
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carcharhinu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gallus gall
                                                                                                                                                            (without alignments)
1061.041 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                     February 22, 2006, 21:24:24; Search time 11.304 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gecko
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P81558
P81558
P061243
P065423
P02688
P02688
P02686
P15728
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Q5nvg4
Q542t4
Q8r4k6
Q6fi04
Q6fi04
Q6fb37
Q5r7j4
P25188
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       2166443 seqs, 705528306 residues
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O542T4 MOUSE
Q8R4K6 RAT
Q6F10 HUMAN
Q6F13 7 HUMAN
Q5F7J4 PONPY
MBP_CAVPO
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QGJ2R3 PIG
QGPK23 HUMAN
MBP RAT
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MBP MOUSE
MBP—HUMAN
MBP—CHICK
O511B1 GECJA
O56972 XENLA
MBP—XENLA
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QSI2C7_BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann Submitted (AUG-2004) to the BMBL/GenBank/DDBJ databases.

GO; GO:0019911; F. Structural constituent of myelin sheath; IEA.
InterPro; IRR000548; Myelin BP.
Pfan; PF01669; Myelin BP; 1.
PRODOM; PD004542; Myelin BP; 1.
PROSITE; PS01669; MYELIN MBP; 1.
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                                                        QSX1V3 | QB33W5 | QB33W5 | QB28d2 | QGGBB7 | QGGBB9 | QGBB1d3 | QGBB1d3 | QGBB1d3 | QGGB1d3 | QGGB528 | QGB528 
Q5wt14
Q86i29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 AA; 8265 MW; ACFE96ACBE9AE551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 AA
                         Q86129_DICDI
QSXIV3_LEGPA
QSXSD2_LEGPA
QSZSD2_LEGPA
Q6D8B7_ERWCT
Q6D8B7_ERWCT
Q6B8B9_9CAUD
Q4ZST7_PSESY
Q8B1D3_PSESW
Q4QAA6_LEINAA
Q7ZXI2_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Amygdala;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 ENPVVHFFKNIVTPRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGAI64_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
Les 17; Conservative
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NCBI_TaxID=9606;
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Last sequence update) Last annotation update)

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NCBI_TaxID=10090;
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Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wakin P.J., McKernan K.J., Malk Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubbs R.A.,
Rahey J., Helton B., Ketteman M., Madan A., Young A.C., Shevichenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Broherztion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Hambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (NOV-2004) to the BBL/GenBank/DDBJ databases.
EMBL, CR26072; CA129699.1; -; mRNA.
EMBL, CR926072; CA129699.1; -; mRNA.
Interpro; IPR000548; Myelin BP.
Ffam; PF01669; Myelin MBP.
Ffam; PF01669; Myelin MBP.
FRINTS; PR0212; WYELINMBP.
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                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BC094522, AAH99522.1; -; mRNA.
InterPro; IRR000548; Myelin BP.
Pfam; PF01669; Myelin MBP; I.
PRINTS; PR00212; MYELINMBP.
Prodom; PD004542; MyeLin BP; 1.
PROSITE; PS00569; MyeLin MBP; 1.
SEQUENCE 128 AA; 1421I MW; 2DAF033C19CF111C CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Name=DKFZp459G2410;
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QSNVG4;
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TISSUE=Brain;
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                               NUCLEOTIDE SEQUENCE
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ARAINECTEM. A. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Awai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S., Arawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ashina M., Batalow S., Casawant T., Radota K., Matsuda H.A., Sabura M., Batalow S., Casawant T., Rabin P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronsetsin M.J., Bult C., Fletcher C., Fullia M., Gariboldi M., Arons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STRAIN=CS7BL/6J; TISSUE=Spinal cord;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kaukiwawa T., Adachi J., Bono H., Kondo S., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Shajdarelli R., Hill D. P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Garriboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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MEDLINE=992A79253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                       Gaps
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Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-58P-2005 (TrEMBLrel. 31, Created)
13-58P-2005 (TrEMBLrel. 31, Last sequence update)
13-58P-2005 (TrEMBLrel. 31, Last annotation update)
Adult male spinal cord cDNA, RIKEN full-length enriched library,
clone:A330079E24 product:myelin basic protein, full insert
                                                                                                                                                                                                                                                       ö
                                                                                                                                                                Score 94; DB 2; Length 150;
Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                  0; Indels
PROSITE; PS00569; MYELIN_MBP; 1.
Hypothetical protein.
SEQUENCE 150 Aa; 16277 MW; AF41CBDB96D8FD01 CRC64;
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                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative 0
                                                                                                                                                                                                                                                                                                                                         1 ENPVWHFFKNIVTPRTP
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Q542T4;
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158 AA

PRT;

Created)

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QBR4K6_RAT PRELIMINARY;
QBR4K6;
                                                                       SOR BERRY REPRESENTATION OF THE PROPERTY OF TH
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A Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
A Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
A Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Mumeta K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
A Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Milming L.G., Wynshaw-Boris A., Carminci P., Hayatsu N.,
A Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carminci P., Hayatsu N.,
A Kiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Pukuda S.,
A Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
A Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
B Hara, H., Barashi, W., Waterston R., Lander E.S., Rogers J.,
B Hara, V. Hansell, V., Lander E.S., Rogers J.,
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C STRAIN-C57BL/GJ; TISSUE-Spinal cord;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Hanagaki T., Hara A., Hashizume W.,
A Huyashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Katoh H., Kawai J., Kojima T., Miyazaki A., Murata M., Nakamura M.,
A Kurhara C., Matsuyama T., Miyazaki A., Murata M., Ohao M., Ohason K., Sano H.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakaume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takahabi F., Takaku-Akahira S., Takada Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUB=Spinal cord;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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Pred. No. 2.2e-07;
Mismatches 0; Indels
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SEQUENCE 154 AA; 17225 MW; 00F1F10ECF90421B CRC64;
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MGI; MGI:96925; Mbp.
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100.0%; Pr
tive 0;
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Matches
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarnhini; Hominidae;
                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley;
MEDLINE=2294925; PubMed=14580679; DOI=10.1016/j.bbaexp.2003.08.010;
Matheus L., Blair G.B.;
"Identification and characterisation of a cDNA encoding a 17-kba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Matheus L.M., Blair G.E.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF439750, AAL84189.1; -; mRNA.

GO; GO:0019911; F: Structural constituent of myelin sheath; IEA.

InterPro; IPR00548; Myelin BP.

PRINTS; PR00212; MYELINMBP.

PROSON: D004842; Myelin BP; 1.

PROSITE; PS00569; MYELINMBP; 1.

SEQUENCE 158 AA; 17240 MW; 3256580242ECC3E1 CRC64;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR536534; CAG38771.1; -; mRNA.
GO; GO:019911; F:structural constituent of myelin sheath; IEA.
InterPro; IPR00548; Myelin BP.
Pfam; PF01669; Myelin MBP; 1.
PRINTS; PR00212; MYELINMBP.
ProDom: P0046542; MyELINMBP.
ProDom: P005659; MYELINMBP; 1.
SEQUENCE 160 AA; 17347 MM; 0107AAD6053CDB76 CRC64;
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                                            Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform of rat myelin basic protein.";
Biochim. Biophys. Acta 1630:47-53(2003)
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01-JUN 2002 (TERMBLEE]. 21,
01-MAR-2004 (TERMBLEE]. 26,
Myelin basic protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 ENPVVHFFKNIVTPRTP
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QEFIO4;
                                                                                                                                                                                                                                                                                                            Muridae; Murinae; Rattus.
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                                                                                                                                                                                                    Rattus norvegicus (Rat).
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100.0%; Score 94; DB 2; Length 160; 100.0%; Pred. No. 2.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                       in experimental autoimmune encephalomyelitis.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                    167 AA.
                               Mismatches
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MEDLINE=84215086; PubMed=6202840;
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                                                                   84 ENPVVHFFKNIVTPRTP 100
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                                                      ENPVVHFFKNIVTPRTP
                                                                                                                                                                                             Myelin basic protein (MBP)
Name=MBP;
       Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                     STANDARD;
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ID MBP C
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                 Gaps
                                                                                                                                                                                                                                                                                              Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J., Submitted (JUV-2004) to the EMBL/GenBank/DDBJ databases. EMBL; CRS41919; CAG4617.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The German CDNA Consortium;

Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger is Pobo G., Han M., Wiemann S.;

Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR860121; CAH92266.1; -; mRNA.

GO; GO:0019911; F:structural constituent of myelin sheath; IEA

InterPro; IPR00548; Myelin BP.

PRINTS; PR00212; MYELIMMBP.

PRINTS; PR00212; MYELIMMBP.
                                                                                                                                                                                                                                                                                                                                                                                            Score 94; DB 2; Length 160; Pred. No. 2.3e-07;
            Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ll protein.
160 AA; 17317 MW; 1A0601CCB257D9C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      160 AA; 17343 MW; 0107AAD603FCD876 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                        Last sequence update)
Last annotation update)
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          100.0%; Score 94; DB 2; I 100.0%; Pred. No. 2.3e-07; ive 0; Mismatches 0;
                                                                                                                                      160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein DKFZp459C0311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD004542; Myelin BP; 1.
PROSITE; PS00569; MYELIN MBP; 1.
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                                                                     1 ENPWHFFKNIVTPRTP 17
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                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 29, CTrEMBLrel. 29, I
                                                                                                                                                            10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, MBP protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pongo pygmaeus (Orangutan)
Ouery Match
Best Local Similarity 100...
Best Local 17; Conservative
                                                                                                                                   QEFH37_HUMAN PRELIMINARY;
QEFH37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSR7J4 PONPY PRELIMINARY;
QSR7J4;
                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2005 (
01-FEB-2005 (
01-FEB-2005 (
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SEQUENCE 16
                                                                               84
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                          Name=MBP
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                                                                                                              RESULT 7
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MEDLINE=76025020; PubMed=51849;
The Contribution of phosphorylation and loss of COOH-terminal
The contribution of the COOH of Market arrangement of the myelin membrane in the COOH as a role in both the formation and stabilization of this compact multilayer arrangement of bilayers.

Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).

CHOBONIT: Homodimer (By similarity).

CHOBONIT: Homodimer (By similarity).

CHOBONIT: Homodimer (By similarity).

CHOBONIT: Homodimer (By similarity).

CHOBONIT: SubCAPTION: Cytoplasmic side of myelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 45-87.
Shapira R., McKneally S.S., Chou F., Kibler R.F.;
"Encephalitogenic fragment of myelin basic protein. Amino acid
"stequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
J. Biol. Chem. 246:4630-4640(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nervous system.

PIPI: At least 5 charge isomers; C1 (the most cationic, least modified, and most abundant form), C2, C3, C4 and C5 (the least cationic form); are produced as a result of optional posttranslational modifications such as phosphory/ation of serine or threonine residues, deamidation of glutamine or apparagine residues, citrullination and methylation of arginine residues. C1 and C2 are unphosphorylated, C3 and C4 are monophosphorylated and C5 is phosphorylated at two positions. SIMILARITY: Belongs to the myelin basic protein family.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 7-156.
STRAIN-BARTIEP; TISSUE-SPINAL cord;
STRAIN-BARTIEP; TISSUE-SPINAL cord;
KIM G., Tanuma N., Matsumoco Y.;
"DNA vaccination using Guinea pig myelin basic protein coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Hystricognathi; Caviidae; Cavia.
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Matches
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MEDLINE=7318037; PubMed=4662101;
Broatcoff S.W., Eylar E.H.;
"The proposed amino acid sequence of the P1 protein of rabbit sciatic
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.MAY-1992 (Rel. 22, Created)
Locy-2001 (Rel. 40, Last sequence update)
13.SEP-2005 (Rel. 48, Last amnotation update)
Myelin basic protein (MBP) (Myelin Al protein) (Myelin Pl protein)
                                                                                                     Direct protein sequencing; Methylation; Myelin; Phosphorylation; Structural protein.
                                                                                                                                                                                                                               Deamidated glutamine (partial) (By similarity).
                                                                                                                                                                                                                                                                Phosphoserine (By similarity).
Citrulline (By similarity).
Deamidated glutamine (partial) (By
                                                                                                                                                                 Phosphoserine (By similarity).
Phosphoserine (By similarity).
Citrulline (By similarity).
Citrulline (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Phosphothreonine (By similarity).
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                                                                                                                              encephalomyelitis (EAE) 1.
Induces experimental autoimmune
encephalomyelitis (EAE) 2.
                                                                                                                         Induces experimental autoimmune
                                 HSSP; PO2686; IQCL.

InterPro.; IPR00548; Myelin BP.

BANTHER; PTHR11429; Myelin BP.

Pfam; PF01669; Myelin MBP; I.

PEDOM; PR0212; MYELINMBP.

PRODOM; PD004549; Myelin BP; I.

PROSITE; PS00549; MYELIN MBP; I.

ACCETYLATION; AUTOIMMUNE encephalomyelitis; Citrullination;
                                                                                                                                                                                                                                              Symmetric dimethylarginine (By similarity).
                                                                                                                                                                                                                                                                                                            Phosphoserine (By similarity). Phosphoserine (By similarity).
                                                                                                                                                                                                                                                                                                                                                      Score 94; DB 1; Length 167; Pred. No. 2.4e-07;
                                                                                                                                                                                                                                                                                                                             Citrulline (By similarity).
866D31F1E5ACFEA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                   Citrulline (By similarity)
                                                                                                                                                            N-acetylalanine
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arch. Biochem. Biophys. 153:590-598(1972)
                                                                                                                                                                                                                                                                                           similarity)
               EMBL; AF074337; AAC26130.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                     18213 MW;
                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                  82 ENPVOHEFKNIVIPRIP
                                                                                                                                                                                                                                                                                                                                                                                          1 ENPVVHFFKNIVTPRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
PROTEIN SEQUENCE OF 45-86.
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                       87
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97
                        PIR; A37246; A37246.
                                                                                                                                                                                                                                                                                                           158
162
167
167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nerve myelin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
MBP_RABIT
ID MBP_RABIT
                                                                                                                                                                                                                                                                                                                  MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=MBP;
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MOD_RES
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                                                                                                                                                                                                           myelin basic protein.",
J. Biol. Chem. 258:390-937(1983).

-! FUNCTION: 18, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splication of this compact multilayer arrangement of bilayers. Each splication in the assembly of an optimized, biochemically functional myelin membrane (By similarity).
-! SUBGUNIT: Homodimer. (By similarity).
-! SUBGURITAR LOCATION: Cytoplasmic side of myelin.
-! TISSUE SPECIFICITY: Found in both the central and the peripheral
                                               human fragments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as a result of optional posttranslatonial modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous system.
PTM: As in other animals, several charge isomers may be produced
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                                                                                                                                                              Martenson R.E., Law M.J., Deibler G.E.; "Identification of multiple in vivo phosphorylation sites in rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Symmetric dimethylarginine (alternate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probom; PD004542; Myelin BP; 1.
PROSITE; PS00569; MYELIN MBP; 1.
Acetylation; Autoimmune encephalomyelitis; Citrullination;
Direct protein sequencing; Methylation; Myelin; Phosphorylation;
Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Omega-N-methylarginine (alternate)
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Deamidated glutamine (partial) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                           Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIM: The N-terminus is blocked.
SIMILARITY: Belongs to the myelin basic protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphoserine.
Phosphoserine (By similarity).
Citrulline (By similarity).
Citrulline (By similarity).
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Deamidated glutamine (partial)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphoserine (By similarity)
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Citrulline (By similarity).
Phosphoserine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encephalomyelitis (EAE).
N-acetylalanine (Probable).
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Citrulline (By similarity).
S -> G (in Ref. 2).
EC3C97ACD2C08EA6 CRC64;
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Shapira R., McKneally S.S., Chou F., Kibler R.F.; "Encephalitogenic fragment of myelin basic protein. sequence of bovine, rabbit, guinea pig, monkey, and J. Biol. Chem. 246:4630-4640[1971].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphoserine.
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                                                                                                                 PHÓSPHORYLATION.
MEDLINE=83108902; PubMed=6185481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; PO2686; 1QCL.
INterPro; IPRO00548; Myelin BP.
BATTHER; PTHR11429; Myelin BP; 1.
Pfam; PPO1669; Myelin MBP; 1.
PRINTS; PRO0212; MYELINMBP.
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18217 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of arginine residues.
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us-10-000-439-13.rup

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Shapira R., McKneally S.S., Chou P.C.-H., Kibler R.F.;
"Encephalicogenic fragment of myelin basic protein. Amino acid
sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
J. Biol. Chem. 246:4630-4640(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pietrowski D., Medugorac I., Foerster M.; "A new MBP allele in Bos taurus is characterized by BseNI PCR-RFLP."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE REVISION.
MEDLINE=14070688; PubMed-4129204;
Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;
Brostoff Cleavage of the Al protein from myelin with cathepsin D.";
J. Biol. Chem. 249:559-567(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE OF 30-42; 74-89 AND 114-129.
MEDLINE=96107211; PubMed=8530487; DOI=10.1074/jbc.270.51.30551;
MEDLINE=96107211; PubMed=8530487; DOI=10.1074/jbc.270.51.30551;
Brasad K., Barouch W., Martin B.M., Greene L.E., Elsenberg E.;
"Purification of a new clathrin assembly protein from bovine brain coated vesicles and its identification as myelin basic protein.";
J. Biol. Chem. 270:30551-30556(1995).
                                                                                                                                                                             MBP_BOVIN STANDARD; PRT; 169 AA.
P02667; Q9BGM8; Q9TS63; Q9TSA6;
P1-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last aquence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa microtubule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bylar B.H., Brostoff S.W., Hashim G., Caccam J., Burnett P., "Basic Al protein of the myelin membrane. The complete amino acid
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pirollet F., Derancourt J., Haiech J., Job D., Margolis R.L.; "Ca(2+)-calmodulin regulated effectors of microtubule stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.";
J. Biol. Chem. 246:5770-5784(1971).
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MEDLINE=72007306; PubMed=5096093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 31:8849-8855(1992)
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                       17
                                            NUCLEOTIDE SEQUENCE OF 4-56.
                       ENPVVHFFKNIVTPRTP
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                                                                                                                                                                                                                                                                                                                   stabilizing protein).
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Sedimentation analysis of the self-association of bovine myelin basic
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98153125; PubMed=9485392; DOI=10.1021/bi972347t;
MEDLINE=98153125; PubMed=9485392; DOI=10.1021/bi972347t;
Zand R., Li M.X., Jin X., Lubman D.;
"Determination of the sites of posttranslational modifications in the charge isomers of bovine myelin basic protein by capillary electrophoresis-mass spectroscopy.";
Biochemistry 37:2441-2449(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system.

PTM: At least 6 charge isomers; C1 (the most cationic and least modified form), C2, C3, C3, C5 and C6 (the least cationic form); are produced as a result of optional posttranslatonial modifications, such as phosphorylation of serine or threonine residues, desmidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.

SIMILARITY: Belongs to the myelin basic protein family.
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Pfam; PF01669; Myelin MBP; 1.
PRINTS; PR00212; MYELINMBP; 1.
PRODOM; PD004542; MYELIN MBP; 1.
PROSITE; P800569; MYELIN MBP; 1.
PROSITE; P800569; MYELIN MBP; 1.
Direct protein sequencing; Methylation; Myelin; Phosphorylation; Structural protein.
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                                                                                                                                                                       PROTEIN SEQUENCE OF 97-104, AND PHOSPHORYLATION SITE THR-97.
MEDLINE=91060584; PubMed=1700979;
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POST-TRANSLATIONAL MODIFICATIONS.
MEDLINE=76167591; PubMed=57115;
Chou F.C. H., Chou C.-H.J., Shapira R., Kibler R.F.;
"Basis of microheterogeneity of myelin basic protein.";
J. Biol. Chem. 251:2671-2679(1976).
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InterPro; IPR000548; Myelin BP
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Pfam; PF01669; Myelin_MBP; 1.
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-!- FUNCTION: Is, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Bach splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).
-!- SUBGNIT: Homodimer (By similarity).
-!- SUBGILULAR LOCATION: Cytoplasmic side of myelin.
-!- SUBCILULAR LOCATION: Cytoplasmic side of myelin.
-!- subcomment of several charge isomers may be produced as a a result of optional posttranslatonial modifications, such as phosphorylation of serine or threonial modifications, such as plutamine or apparagine residues, citrullination and methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=76009821; PubMed=51459; DOI=10.1016/0024-3205(75)90506-8; Westall F.C., Thompson M., Kalter S.S.; "The proposed sequence of the encephalitogenic protein from chimpanzee
                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                      Gaps
Citrulline (By similarity).
Citrulline (By similarity).
Phosphoserine (in C4, C5 and C6).
Phosphoserine (By similarity).
Phosphothreonine (by MAPK) (in C3, C4, and C6).
                                                                                   Omega-N-methylarginine (alternate).
Symmetric dimethylarginine (alternate).
Phosphoserine (By similarity).
                                                                                                                    Citrulline (By similarity).
Desmidated glutamine (in form C2).
Citrulline (By similarity).
Phosphoserine (in C4 and C6).
Phosphoserine (in C3, C5 and C6).
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                                                                         Deamidated glutamine (in form CS
                                                                                                                                                                                                             Score 94; DB 1; Length 169;
Pred. No. 2.4e-07;
Mismatches 0; Indels
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                                                                                                                                                                             Citrulline (Probable)
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Last annotation update)
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InterPro; IPR000548; Myelin_BP.
PANTHER; PTHR11429; Myelin_BP; 1.
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PRELIMINARY PROTEIN SEQUENCE.
                                                                                                                                                                                                                          100.08;
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10-MAY-2005 (Rel. 47, Last
Myelin basic protein (MBP)
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Best Local Similarity 100.
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169 AA;
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MBP_PANTR
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Kira J.-I., Deibler G.E., Krutzach H.C., Martenson R.E.;
J. Neurochem. 44:1653-165(1985).

-!- FUNCTION: 18, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCLIULIAR LOCATION: Cytoplasmic side of myelin.
-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslatonial modifications, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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PRINTS; PR00212; MYELINMBP.
Prodom; PD004542; Myelin BP; 1.
PROSITE; PS00569; MYELIN MBP; 1.
Acetylation; Autoimmune encephalomyelitis; Citrullination;
Direct protein sequencing; Methylation; Myelin; Phosphorylation;
Structural protein.
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                                                                                                                                                                                                                                                            Phosphothreonine (By similarity)
Deamidated glutamine (partial) (
                                                                                                                  N-acetylalanine.
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Citrulline (By similarity).
Citrulline (By similarity).
Phosphoserine (By similarity).
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Phosphoserine (By Similarity)
Phosphoserine (By Similarity)
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MEDLINE=85056964; PubMed=2578056;
Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;
"Amin acid sequence of porcine myelin basic protein.";
J. Neurochem. 44:134-142(1985).
                                                                                                                                                                                                                                                                                                   similarity).
Omega-N-methylated arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Citrulline (By similarity)
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E9FED59DE6933293 CRC64;
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100.0%; Pred. No. 2.5e-07;
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Last annotation update)
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(Rel. 39, Last sequ
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P81558; P98189;
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SEQUENCE
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Query Match
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                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                            PIR; A61640; MBPGB.

R HSSP; P02686; 10CL.

R HSSP; P02686; 10CL.

R HSSP; P02686; 10CL.

R PANTHER; PTHR11429; Myelin BP.

R PRINTS; PR001512; MYELIN MBP; 1.

R PRINTS; PR00569; MYELIN MBP; 1.

R PROSTTE; P800569; MYELIN MBP; 1.

R PROSTTE; P800569; MYELIN MBP; 1.

R Acetylation; Citrullination; Direct protein sequencing; Methylation; Myelin; Phosphorylation; Structural protein.

W Myelin; Phosphorylation; Structural protein.

W Myelin; Phosphorylation; Structural protein.

W MOD_RES 1 N-acetylalanine.

W MOD_RES 12 25 Citrulline (By similarity).

T MOD_RES 25 Phosphoserine (By similarity).

T MOD_RES 55 Phosphoserine (By similarity).

T MOD_RES 98 98 Phosphothreonine (By similarity).

T MOD_RES 103 103 Phosphoserine (By similarity).

T MOD_RES 103 103 Phosphoserine (By similarity).

T MOD_RES 103 103 Phosphothreonine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name-DKFZp459C0215; Synonyms-DKFZp459P2220;
Name-DKFZp459C0215; Synonyms-DKFZp459P2220;
Pongo pygmaeus (Orangutan).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Omega-N-methylarginine (alternate).
Symmetric dimethylarginine (alternate).
Phosphoserine (By similarity).
Deamidated glutamine (partial) (By
phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 94; DB 1; Length 171; 100.0%; Pred. No. 2.5e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphoserine (By similarity).
Phosphoserine (By similarity).
                               of arginine residues.
SIMILARITY: Belongs to the myelin basic protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSR618;

05R618;

01-FEB-2005 (TrEMBLrel. 29, Created)

01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

Hypothetical protein DKFZp459C0215 (Hypothetical protein DKFZp459F2220).
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The German cDNA Consortium;
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Matches 17; Conserv
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.K.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR860682; CAH92798.1; -; mRNA.

GO, GO:0019911; F:structural constituent of myelin sheath; IEA.

InterPro; IPR000548; Myelin BP.

Pfam; PR01669; Myelin BP; 1.

PRODOM; PR01612; Myelin BP; 1.

PRODOM; PR004542; Myelin BP; 1.

PRODOM; PR00569; MXELIN BP; 1.

Hypothetical protein.

EMBS650306305540 CRC64;
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EMBL; AX603684; AAT28338.1; -; mRNA.

EMBL; AX603684; AAT28338.1; -; mRNA.

EO; GO:019911; F: Structural constituent of myelin sheath; IEA.

EO; GO:019911; F: Structural BP.

Pfam; PF01669; Myelin MBP; 1.

PRINTS; PR00212; MYELINMBP.

ProDom; PD004542; Myelin BP; 1.

PR051TE; PS00569; MYELIN BP; 1.

SEQUENCE 173 AA; 18731 MW; 6684D016E66081AA CRC64;
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PubMed=15771731; DOI=10.1111/j.1365-2052.2005.01236.x;
Rim J.G., Nonneman D., Vallet J.L., Rohrer G.A., Christenson
"Linkage mapping of the porcine myelin basic protein gene to chromosome 1.";
                                                                                                                                                                                                                                                                                                    100.0%; Score 94; DB 2; Length 171;
100.0%; Pred. No. 2.5e-07;
ive 0; Mismatches 0; Indels
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Last annotation update)
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Best Local Similarity 100.
Matches 17; Conservative
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1es 17; Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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(without alignments) 944.229 Million cell updates/sec

US-10-000-439-13 94 1 ENPVVHFFKNIVTPRTP 17 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

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94 100.0 128 1 MBRTS 94 100.0 167 2 A37246 94 100.0 167 2 A37246 94 100.0 171 1 MBPGB 94 100.0 171 1 MBPGB 94 100.0 171 1 MBPGB 94 100.0 328 1 MBMSB 87 92.6 174 2 808535 60 63.8 128 2 A60215 53.8 128 2 A60215 54 47.9 308 2 G64449 44 46.8 639 2 A45246 44 46.8 639 2 A45246 44 46.8 639 2 A62246 44 45.7 114 2 S12904 43 45.7 114 2 S12904 44 45.7 1124 2 B84742 44 45.7 1124 2 B84742 44 45.7 1124 2 B84742 44 47 435 2 AG1541 41 43.6 332 2 A73308 41 43.6 332 2 A73308 41 43.6 690 2 A11174 41 43.6 590 2 A11174	sult No.	Score	Quer	y h Lengtl			Description
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hypothetical prote	hypothetical prote	cytosine/guanine d	probable peptide m	probable ribonucle	hypothetical prote	ATM-like protein [hypothetical prote	protein F41H10.2 [glutamate racemase	hypothetical prote	hypothetical prote	C4-dicarboxylate-b	conserved hypothet	conserved hypothet	o-succinylbenzoate
T27005	AD2530	D96934	T50177	H72510	T51040	C85426	T05501	F88690	B81262	F86897	T15311	S18578	F89944	H70302	AB0308
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892	192	428	431	983	1162	2089	3738	164	250	270	323	333	337	431	471
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43	42	42.6	42	42	42	42	42	41	41	41	41	41	41	41	41
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ALIGNMENTS

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		protein
-		basic
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NyAlternate names: small myelin basic protein
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: B24351; A264243; A21062; A03142
R;Schaich, M.; Budzinski, R.M.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 825-834, 1986
A;Title: Cloned proteolipid protein and myelin basic protein cDNA. Transcription of the A;Reference number: A24351; MUID:87026249; PMID:2429678

A; Molecule type: mRNA
A; Residues: 1-128 «SCH»
A; Residues: 1-128 «SCH»
A; Residues: 1-128 «SCH»
A; Cross-references: UNIPROT: P02688; UNIPARC: UPI0000163B8F; EMBL: M25889; NID: g205321; PI: R; Dunkley, P.R.; Carnegie, P.R.
Biochem. J. 141, 243-255, 1974
A; Title: Amino acid sequence of the smaller basic protein from rat brain myelin.
A; Réference number: A90275; MUID: 75127359; PMID: 4141893

A;Accession: A90275
A;Molecule type: protein
A;Residues: 2-128 cDUN.
A;Cross-references: UNIPARC:UP1000022ADB4
A;Cross-references: UNIPARC:UP1000002ADB4
A;Note: at position 105, arginine, monomethylarginine, and dimethylarginine occur in th
A;Note: rats have two myelin basic proteins; the smaller one, shown above, is missing 4:
A;Note: rats have two myelin basic proteins; the smaller one, shown above, is missing 4:
B;Note: plant, D.E.; Blank, S.E.; Kibler, R.F.; McKneally, S.; Shapira, R.
Science 179, 478-480, 1973
A;Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogen:
A;Reference number: A94243; MUID:73180720; PMID:4122324

A; Accession: A94243

A; Molecule type: protein
A; Residues: 46-86 < MCF.
A; Residues: 46-86 < MCF.
A; Cross-references: UNIPARC: UP100001740CC
A; Note: the sequence reported for this encephalitogenic peptide differs from that shown
R; Roach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.B.
A; Title: Characterization of cloned cDNA representing rat myelin basic protein: absence
A; Reference number: A21062; MUID:84026484; PMID:6194889

A; Molecule type: mRNA

A;Redidues: 1124, 17,126-128 cROA>
A;Cross-references: UNIPARC:UP1000002E780
A;Cross-references: UNIPARC:UP1000002E780
A;Experimental source: strain Sprague-Dawley
C;Superfamily: myelin basic protein
C;Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalom;
C;Keywords: myelin basic protein % #status experimental autoimmune encephalom;
F;2.128/Product: myelin basic protein % #status experimental cMAT>
F;2.106/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #stat:
F;105/Modified site: omega-N-methylarginine or omega-N,omega-N,-dimethylarginine (Arg)

ô Query Match 100.0%; Score 94; DB 1; Length 128; Best Local Similarity 100.0%; Pred. No. 9.6e-09; Matches 17; Conservative 0; Mismatches 0; Indels

Gaps ö

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A;Cross-references: UNIPARC:UP100001740BD
R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in gli
A;Reference number: S54343; MUID:95194333; PMID:7887910
A;Accession: S54343
                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Molecule type: protein
A; Residues: 74-75, 'HG, '78-82,'D', '84-88;105,'X',107-108,'X',110-114,'X',116-119 <OKA>
A; Creatules: 74-75,'HG,'T8-82,'D', '84-88;105,'X',107-108,'X',110-114,'X',116-119 <OKA>
A; Creatules: 74-75,'HG,'T8-80,'T8-80,'T8-80,'X', Tatemoto, K.
B; Takamatsu, K.; Tatemoto, K.
Neurochem. Res. 17, 239-246, 1392
Neurochem. Res. 17, 239-246, 1392
A; Title: Isolation and characterization of two novel peptide amides originating from my: A; Reference number: A61641; MUID:92319189; PMID:1377792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1-16 - CTA2.
A; Residues: 1-16 - CTA2.
A; Cross-references: UNIPARC:UPI00001740C0
A; Residues: 1-16 - CTA2.
A; Cross-references: UNIPARC:UPI00001740C0
A; Note: these peptides have carboxyl-terminal amides probably produced by a non-enzymat R; Brostoff, S.; Eylar, E.H.
B; Proco. Natl. Acad. Sci. U.S.A. 69, 765-769, 1971
A; Title: Localization of methylated arginine in the Al protein from myelin.
A; Reference number: A93777; MUID:71153946; PMID:4994464
A; Contents: annotation
A; Reference number: A3777; MUID:71153946; PMID:4994464
A; Note: Arg-106 is modified to monomethylarginine and dimethylarginine
B; Eylar, E.H.; Caccam, J.; Jackson, J.J.; Westall, F.C.; Robinson, A.B.
Science: 168, 1220-1223, 1970
A; Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site of A; Reference number: A94241; MUID:70178977; PMID:5442707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Contents: annotation
A; Contents: annotation
A; Note: the region including residues 114-122 induces experimental allergic encephalomy,
A; Note: the region including residues 114-122 induces experimental allergic encephalomy,
C; Superfamily: myelin basic protein
E;1-169/Product: myelin basic protein #status experimental <AMI>
F;1-16/Product: myelin peptide amide-12 #status experimental <PAI>
F;1-12/Product: myelin peptide amide-12 #status experimental <PAI>
F;1-12/Product: myelin peptide amide-12 #status experimental <PAI>
F;1-12/Product: myelin peptide amide-12 #status experimental <PAI>
F;1-16/Modified site: acetylated amino end (Ala) #status experimental
F;16/Modified site: amidated carboxyl end (Tyr) [amide in mature form myelin peptide am F;16/Modified site: omega-N-methylarginine or omega-N, omega-N'-dimethylarginine (Arg)
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A; CCOmment: This protein may function in maintaining the proper structure of myelin.
C; Comment: This protein basic protein
C; Superfamily: myelin basic protein
C; Keywords: blocked amino end; methylated amino acid; myelin; structural protein
F; L/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
F; 107/Modified site: omega-N-methylarginine or omega-N, omega-N, -dimethylarginine (Arg)
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C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A03139
R;Westerall, FC.7; Thompson, M.; Kalter, S.S.
Life Sci. 17, 219-223, 1975
A;Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.
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N,Alternate names: MBP
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A; Realdues: 1-169 <BRO.
A; Creatdues: 1-169 <BRO.
A; Creatdues: 1-169 <BRO.
B; Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
J. Biol. Chem. 246, 4630-4640, 1971
A; Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin
A; Reference number: A92087
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J. Biol. Chem. 246, 4630-4640, 1971
A;Tille: Bncephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin A;Reference number: A92087
A;Accession: C92087
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                                                                                                                                                                                                                                                                                                                                                 myelin basic protein - guinea pig
NyAlternate names: myelin Al protein
C'Species: Cavia myelin Al protein
C'Species: Cavia porcellus (guinea pig)
C'Species: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
C'Accession: A37-246; C92087; Ã03140
S'R.Jeblar, G.E.; Martenson, R.E.; Krutzsch, H.C.; Kies, M.W.
J. Neurochem. 43, 100-105, 1984
A'Title: Sequence of guinea pig myelin basic protein.
A'Reference number: A37246; MUID:84215086; PMID:6202840
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A; Residues: 1, %, 2-169 «EXL»
A; Cross-references: UNIPROT: P02687; UNIPARC: UPI0000148533
R; Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.
J. Biol. Chem. 249, 559-567, 1974
A; Title: Specific cleavage of the Al protein from myelin with cathepsin l
A; Reference number: A92160; MUID: 74070688; PMID: 4129204
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A,Molecule type: protein
A,Residues: 1-17 <DEL>
A,Crosg-references: UNIPROT:P25188; UNIPARC:UP1000012ED39
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Pred. No. 1.3e-08;
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C;Superfamily: myelin basic protein
C;Keywords: myelin
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Best Local Similarity 100.0
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Gaps

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A;Accession: A94106
A;Molecule type: mRNA
A;Residues: 1-59,86-197 <KAM>
A;Cross-references: UNIPARC:UPI000002ADA6; GB:M13577; NID:G187408; PIDN:AAA59562.1; PID
A;Notes: 18.5K splice form
A;Accession: B94106
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A; Residues: 2-59,86-197 cPRO>
A; Residues: 2-59,86-197 cPRO>
A; Cross-references: UNIPARC: UP10000113626
A; Cross-references: Universe brain
B; Scoble, H.A.; Whitaker, J.N.; Biemann, K.
A; Neurochem, 47, 614-616, 1986
A; Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44 an A; Reference number: A60862; MUID:86280476; PMID:2426402
A; Accession: A60862
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. Blol. Chem. 264, 5121-5127, 1989
Title: The isolation, characterization, and lipid-aggregating properties of a citrull'
Reference number: A33273; MUID:89174797; PMID:2466844
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Affile: Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a new form of
A;Reference number: 154219; MUID:90152679; PMID:1689270
A;Accession: 114219
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R;Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.B.; Prusiner, S.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encephalitogens from human myelin bas
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R;Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.
Biol. Chem. 259, 5028-5031, 1984
A;Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined
A;Reference number: A61420; MUID:84185608; PMID:6201481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a 17.2K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. J. 123, 57-67, 1971
A;Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.
A;Reference number: A90256; MUID:72066400; PMID:4108501
A;Accession: A90256
                   cDNA cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UP1000002ADA4
A;Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form A;Note: a 17.2K splice form is also described
A;Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form;
R;Carnegie, P.R.
A;Title: Identification of three forms of human myelin basic protein by A;Reference number: A94106; MUID:86259714; PMID:2425357
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A;Residues: 2-45;117-197 <SCO>
A;Cross-references: UNIPARC:UP100001740B8; UNIPARC:UP100001740B9
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Biochem Biophys. Res. Commun. 192, 1175-1181, 1993
A;Title: Leukocyte gelatinase B cleavage releases enceph
A;Reference number: JH0802; MUID:93282820; PMID:7685161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 2-59,86-197 <CAR>
A;Cross-references: UNIPARC:UP10000113626
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A,Residues: 46-59,86-116 <GIB>
A,Cross-references: UNIPARC:UP100001740BA
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A; Residues: 1-197 < KA2>
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C;Species: Homo sapiens (man)
C;Date: 18-Dec-1981 #sequence revision 25-Aug-1995 #text change 09-Jul-2004
C;Date: 18-Dec-1981 #sequence revision 25-Aug-1995 #text change 09-Jul-2004
C;Accession: 810482; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; I54219; I56
R;Streicher, R; Stoffel, W.
Biol. Chem. Hoppe-Seyler 370, 503-510, 1989
A;Title: The organization of the human myelin basic protein gene. Comparison with the mc
A;Reference number: S10482; MUID:89302693; PMID:2472816
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A;Residues: 1-197 <STR.
A;Residues: 1-197 <STR.
A;Cross-treferences: UNIPROT:P02686; UNIPARC:UPI000002ADA4; EMBL:X17286; NID:G34490; PIDN
B;Kamholz, J.; De Ferra, F.; Puckett, C.; Lazzarini, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986
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N;Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein pred
.5K splice form
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N.Alternate names: myelin Al protein
N.Contains: myelin basic protein amide 14
N.Contains: myelin basic protein amide 14
C.Species: Sus scrofa domestic domestic pig)
C.Date: 19-Apr-1996 #sequence_revision 26-Apr-1996 #text_change 09-Jul-2004
C.Accession: A61640; A36245
R.Kira, J.: Deibler, G.E.; Krutzsch, H.C.; Martenson, R.E.
J. Neurochem, 44, 134-142, 1985
A.Title: Amino acid sequence of porcine myelin basic protein.
A.Reference number: A61640; MUID: 85056964; PMID: 2578056
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Pred. No. 1.3e-08;
Mismatches 0; Indels
                                                               Length 171;
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                                                Query Match
100.0%; Score 94; DB 1; I
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 0;
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100.0%; Score 94; DB
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 17; Conservative 0; Mismatches
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A;Reference number: A45421; MUID:93186801; PMID:7680345
A;Accession: A45421
A;Molecule type: mRNA
A;Residues: 1-190;217-75;316-328 <CAMI>
A;Cross-references: UNIPROT:P04370; UNIPARC:UPI00001740C3; UNIPARC:UPI00001740C4; UNIPARA;Experimental source: clone J37
A;Note: sequence extracted from NCBI backbone (NCBIN:126696) and modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: sequence extracted from NCBI backbone (NCBIN:126700, NCBIP:126715)
R; de Farrar, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molineaux, S.; Lazzarin:
Cell 43, 721-727, 1985
A; Title: Alternative splicing accounts for the four forms of myelin basic protein.
A; Reference number: A90875; MUID:86079555; PMID:2416470
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A, Experimental source: 18.5K
R, Memman, S.; Kitamura, K.; Campagnoni, A.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987
A, Title: Identification of a cDNA coding for a fifth form of myelin basic protein in mon A, Recession: A26591
A, Accession: A26591
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A; Residues: 134-274;316-328 <NEW1>
A; Residues: 134-274;316-328 <NEW1>
A; Cross-references: UNIPARC:UPI00001740C5; UNIPARC:UPI00001740C8; GB:M15060; NID:G19904.
A; Experimental source: clone M722; splice form 17.22K
A; Accession: B26591
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 134-328 <a href="https://doi.org/10.200002ADA9">https://doi.org/10.200404</a>; GB:L00404; GB:M11669; NID:g199060; PIDN:AAA3
A;Experimental source: 21.5K
A;Experimental source: 21.5K
Cell 42, 139-148, 1985
A;Title: Cloning and characterization of the myelin basic protein gene from mouse: one A;Reference number: A90867; MUID:85254913; PMID:2410136
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A;Residues: 1-191, SSEP' <CAM2>
A;Cross-references: UNIPARC:UP10000004029; GB:L07508; NID:g193586; PIDN:AAA37721.1;
A;Experimental source: clone BG21
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R;Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A. Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984
A;Title: Characterization of mouse myelin basic protein messenger RNAs with a A;Reference number: I58996; MUID:84119431; PMID:6198644
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A; Residues: 134-190; 217-274; 316-328 < KIT>
A; Residues: 134-190; 217-274; 316-328 < KIT>
A; Crosar references: UNIPARC: UPIO0001740C5; UNIPARC: UPIO0001740C6; UNIPARC: UPIO0001740C6; UNIPA; Sxperimental source: M41; splice form 14K
B; Grima, B.; Zelenika, D.; Pessac, B.
J. Neurochem, 59, 2318-2323, 1992
A; Title: A novel transcript overlapping the myelin basic protein gene. A; Reference number: 148407; MUID: 93057537; PMID: 1279125
A; Accession: 148407
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-191,'SSEP' <GRI>
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A; Status: preliminary
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C, Superfamily: myelin basic protein
C, Superfamily: myelin basic protein
C, Keywords: acetylated amino end; alternative splicing; citrulline; experimental autoimm
E, 2-132, 1947/Product: myelin basic protein, 21.5K splice form #status predicted «MAT2
F, 2-132, 144-197/Product: myelin basic protein, 18.5K splice form #status experimental «MAT
F, 2-59, 86-132, 144-197/Product: myelin basic protein, 18.5K splice form #status predicted
F, 2/Modified site: acetylated amino and (Ala) (in mature form) #status experimental
F, 26, 32, 149, 157, 186, 197/Modified site: citrulline (Arg) (in form C-8) #status experiment
F, 134/Modified site: omega-N-methylarginine or omega-N, omega-N'-dimethylarginine (Arg) (
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N;Alternate names: golli-mbp protein; MBP
N;Contains: myelin basic protein; MBP
N;Contains: myelin basic protein;
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A45421; B45421; A50875; A90867; A26591; B26591; A60920; I48407; I58996; I54
R;Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Landry, J. Biol. Chem. 268, 4930-4938, 1993
A;Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase gene that e
                                                                                                                                 A;Cross-references: UNIPARC:UPI000016AD10; GB:M63599; NID:9187402; PIDN:AAA59560.1; PID: R;Roth, H.J.; Kronquist, K.E.; Kerlero de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T. J. Neurosci. Res. 17, 321-328, 1987
A;Title: Evidence for the expression of four myelin basic protein variants in the develon A;Reference number: I56567; MUID:87311781; PMID:2442403
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: Molecule type: Mo
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A;Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin A;Reference number: I56565; MUID:86308101; PMID:2427738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPARC:UP1000002ADA5; GB:M30516; NID:g187410; PIDN:AAA59563.1; PID
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A;Cross-references: UNIPARC:UP100001740BC
C;Comment: Four alternatively spliced forms of myelin basic protein have been observed,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-132,144-197 <RB2> A;Cross-references: UNIPARC:UF1000002ADA5; GB:M30510 A;Accession: I73634 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: mRNA; Residues: 1-197 <RE3>
preliminary; translated from GB/EMBL/DDBJ
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Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3
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Matches
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C'Species: Heterodontus francisci (horn shark)
C'Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change 09-Jul-2004
C'Accession: B3299
B'Saavedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, A. Mol. Bvol. 29, 149-156, 1989
A'Title: The myelin proteins of the shark brain are similar to the myelin proteins of the A;Reference number: A32999; MUID:90040744; PMID:2478717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-155 <SAA>
A;Cross-references: UNIPROT:P20939; UNIPARC:UPI00001713F7; GB:X17664; NID:g63974; PIDN:C
C;Superfamily: myelin basic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nypotherical protein MJ1128 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Accession: G64440
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R;Bult, C.J.; Warbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.:
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; A;Reference number: A64300; MUID:96337999; PMID:8688087
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myelin basic protein - dusky shark (fragments)
C;Species: Carcharhinus obscurus (dusky shark)
C;Accession: A60215
R;Milne, T.J.; Atkins, A.R.; Warren, J.A.; Auton, W.P.; Smith, R.
J. Neurochem: S5, 950-955, 1990
A;Title: Shark myelin basic protein: amino acid sequence, secondary structure, and shittle: Shark myelin basic protein: A6190347482; PMID:1696624
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                                                                                                                                                                                                                                                                                                     A,Accession: A60215
A;Molecule type: protein
A;Residues: 1-128 <MIL.>
A;Residues: 0.128 <MIL.>
A;Cess-treferes: UNIPROT:P98190; UNIPARC:UPI0000FDE5C
A;Note: the source was designated as Carcharhinus obscurus (whaler shark)
C;Superfamily: myelin basic protein
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Pred. No. 0.0065;
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Pred. No. 0.13;
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C;Superfamily: hypothetical protein MJ1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
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A,Map position: REV1069975-1069049
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DSAVVHFFKNMMSPK 86
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Best Local Similarity 53.3.
Best Local 8, Conservative
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Best Local Similarity 52.9
Matches 9; Conservative
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A;Status: preliminary
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Gene organization and transcription of duplicated MBP genes of myelin deficient A,Reference number: 153256; MUID:88196094; PMID:2452084
A,Reference number: 153256; MUID:88196094; PMID:2452084
A,Reference number: 153256
A,Status: translation not shown; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 217-229, 'MN',232-250 <OKA>
A,Residues: 217-220, 'MN', 232-250 <OKA, 273-220, 'MN', 232-250 <OKA, 273-220, 'MN', 232-250 <OKA, 273-220, 'MN', 232-200 <OKA, 273-220, 'MN', 232-200 <OKA, 273-220, 'MN', 232-200 <OKA, 273-220, 'MN', 232-220, 'MN', 232-
                                   A, Residues: 219-248 <2EL>
A, Rossidues: 219-248 <2EL>
A, Grose-references: UNIPARC: UPI000016CED2; GB: K00989; NID: G199037; PIDN: AAA39495.1; PID: R, Miura, M.; Tamura, T.
Gene 75, 31-38, 1989
A, Title: The promoter elements of the mouse myelin basic protein gene function efficient A, Reference number: 154033; MUID: 89252919; PMID: 2470651
A, Accession: 154033
A, Accession: 154033
A, Molecule type: DNA
A, Residues: 134-157 <MIU>
A, Residues: 134-157 <MIU>
B, Residues: 134-157 <MIU>
B, Crose-references: UNIPARC: UPI000016CED5; GB: M24410; NID: G199052; PIDN: AAA39498.1; PID: R, Okono, H.; Tamura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K. EMBO J. 7, 77-83, 1988
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C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Osul-2004
C.Accession: S08535
R.Zopf, D.; Sonntag, V.; Betz, H.; Gundelfinger, E.D.
Gila 2, 241-249, 1989
A.Title: Developmental accumulation and heterogeneity of myelin basic protein transcript A.Reference number: S08535
A.Rocession: S08535
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: MRNA
A.Residues: 1-174 < ZOP>
A.Coperfamily: Myelin basic protein
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
Matches 17; Conserv
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Search completed: February 22, 2006, 21:38:18 Job time : 2.7323 secs
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C; Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C; Accession: 146577
R; Baker, D.L.; Paietta, J.V.
Submitted to the EMBL Data Library, February 1997
A; Description: Molecular characterization of the arylsulfatase gene of Neurospora crassa
A; Reference number: 223090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 7
A;Introns: 115/1; 518/3
C;Function: A;Description: EC 3.1.6.1 [validated, MUID:89384589]
A;Description: EC 3.1.6.1 [validated, MUID:89384589]
C;Superfamily: arylsulfatase, plant type
C;Keywords: 8ulfuric ester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: A57246
A,Status: preliminary
A,Molecule type: mRNA
A,Molecule: 1-329 <KILb
A,FCOSS-references: UNIPROT:P54097; UNIPARC:UPI0000136B89; GB:L38519; NID:g602439; PIDN:C;Keywords: extracellular matrix; membrane protein; phosphatidylinositol linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-639 <BAK>
A;Residues: 1-639 <BAK>
A;Crose-references: UNIPROT:O43113; UNIPARC:UP1000006B2E2; EMBL:U89492; PIDN:AAC02716.1
A;Experimental source: strain wild type 74-OR23-1A
C;Genetics:
                                                                                                                                                                                                                                                                             C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57246
R;Killick, R.; Legan, P.K.; Malenczak, C.; Richardson, G.P.
J. Cell Biol. 129, 535-547, 1995
A;Title: Molecular cloning of chick beta-tectorin, an extracellular matrix molecule of A;Reference number: A57246; MUID:95238547; PMID:7721949
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                                                                                                                                                                                                                                beta-tectorin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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Length 308;
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S12904
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
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DB 2;
6.7;
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Pred. No. 11;
4; Mismatches
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Pred. No. 23;
Score 45; DB 2
Pred. No. 6.7;
2; Mismatches
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47.9%;
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53.8%;
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Best Local Similarity 50.0%;
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Best Local Similarity 53.87
Conservative
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HLFPDVIVPRTP 293
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Matches 7; Conserv
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C;Species: Pisaster ochraceus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Datesion: S12904
R;Sanghera, J.S.; Abbersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FBBS Lett. 273, 223-226, 1990
A;Title: Identification of the sites in myelin basic protein that are phosphorylated by A;Reference number: S12904; MUID:91032186; PMID:1699809
A;Accession: S12904
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <SAN>
A;Cross-references: UNIPROT:Q7M3M4; UNIPARC:UPI000017BF0C
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Štaphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C99965
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu: ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <KUR>
A;Cross-references: UNIPROT:Q99T75; UNIPARC:UPI000013B193; GB:BA000018; PID:g13701588;
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45.7%; Score 43; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 35.7%;
Matches 5; Conservative
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February 22, 2006, 21:24:11; Search time 11.1572 Seconds (without alignments) 669.475 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1 ENPVVHFFKNIVTPRTP 17
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1: geneseqp1990s:*
2: geneseqp1990s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay69395 Peptide d	Aao20308 Myelin ba	Aae26359 Peptide r	Aae23935 Peptide a	Abp97941 Amino aci	Abr56063 Glycopept	Aao19672 Human mye	Ade50773 Wild-type	Adw36476 HLA bindi	Adw35045 HLA bindi	Adw33812 HLA bindi	Adk67704 Human mye	Adl18291 Human mye	Aeb77584 MBP pepti	Aeb86495 Myelin ba	Aar44115 Human mye	Aar95357 Residues	Aaw73600 Human mye	Aay66533 Myelin ba	ı,	Aar44114 Human mye	Aar44123 Human mye	Aar85132 Human MBP	Aaw05719 Residues
SUMMARIES	QI	AAY69395	AA020308	AAE26359	AAE23935	ABP97941	ABR56063	AA019672	ADE50773	ADW36476	ADW35045	ADW33812	ADK67704	ADL18291	AEB77584	AEB86495	AAR44115	AAR95357	AAW73600	AAY66533	AAR32295	AAR44114	AAR44123	AAR85132	AAW05719
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AAR95366 AAR95356 AAR95356 AAR95356 AAW34183 AAW34180 AAW44071 AAW73616 AAX58992 AAX58992 AAX88550 AAX66532 AAX66532 AAX66512613 AAM5612613 AAM5612613 AAM5612613 AAM5612613 AAM665171	ALIGNMENTS AA.			myelin basi	oligodendrogli multiple scler						ERW GES INC.			ω <u>μ</u>	2pp; English.	a per four analc atier alls are
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	; peptide;		rst entry)	from a h	prc anal				9WO-US0190	8US-001377	S AG. S-ERFINDUNGEN VERW G) INE BIOSCIENCES INC.	, Ling	19.	: immune response ic protein, MBP, o iple sclerosis, by ys of MBP.	; 112pp	The present sequence represents a protein. Myelin basic protein is oligodendroglial cells. Peptide a sequence are administered to a piresponse (i.e. production of T or cytokines) and/or a persistent syprotein. These peptide analogues derived from residues 83-99 of h
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The present invention relates to a novel method for inducing Th2 immune responses to Myelin Basic Protein (MBP) or a peptide analogue of MBP in a patient. The method involves administering a composition comprising the MBP peptide analogue CGP 77116 (NBI-5788). The method is useful for treating multiple sclarosis (MS). Sequences of the invention are also used as vaccines. The present sequence is a peptide related to human MBP
of the invention of peptide region 83-99 of Myelin basic protein (MBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducing Th2 immune responses to Myelin Basic Protein (MBP) by administering the MBP peptide analog CGP 77116, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The immune response, myelin basic protein, MBP; vaccine, MS; multiple sclerosis; antisclerotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for selecting a tolerogenic peptide, comprising selecting a peptide which is capable of binding to a major histocompatibility complex (MHC) class I or II molecule without further processing. The peptides of the invention are useful for preventing a disease such as hypersensitivity disorder, and also for treating and/or preventing a disease. In a subject. The method involves identifying an antigen for the disease, identifying an apitope (antigen processing independent epitope) for the antigen, and administering the apitope to the subject. The peptides of the invention are also useful for treating allergies such as extrinsic asthma, atopic dermatitis, allergic rhinitis, utricaria, autoimmune diseases such as multiple sclerosis, autoimmune transmers and such as multiple sclerosis, autoimmune transmers, systemic sclerosis, arcoidosis, autoimmune transmit polymyositis, diabetes, etc, and transplant rejection. The peptides are also useful for modifying antiviral CD8+ responses in a tolerogenic fashion. This sequence represents an apitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological, antiallergic, neuroprotective; antithyroid; antianaemic; vasotropic, antinflammatory; immunosuppressive; antidiabetic; class I; major histocompatibility complex; MHC; class II; autoimmune thyroiditis; hypersensitivity disorder; antigen; allergy; extrinsic asthma; utricaria; autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis; autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis; systemic sclerosis; polymyositis; diabetes; transplant rejection;
    positions 91, 95 or 97. The peptide treatment of multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myelin basic protein; apitope; antiasthmatic; tolerogenic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Selecting tolerogenic peptide useful for treating autoimmune diseases e.g. multiple sclerosis, involves selecting peptide which binds major histocompatibility complex class I or II molecule without further
                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streeter HB;
                                                                                                        Score 94; DB 3; Length 17;
Pred. No. 7e-09;
                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myelin basic protein (MBP) apitope peptide region 83-99.
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                                                                                                                                                    Mismatches
    from the native sequence at least at analogs are especially useful in the
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                                                                                                                                                                                                                                                                                                                                         AAO20308 standard; peptide; 17
                                                                                                          100.0%;
                                                                                                                                                                                                                   ENPVVHFFKNIVTPRTP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                            Local Similario,
nes 17; Conservative
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                                                                 Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiviral CD8+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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Length 17; 0; Indels

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Immunoabsorption column, useful for treating multiple sclerosis, contains glycopeptides able to react with disease-specific autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                     containing conjugates comprising glycopeptides which are able to recognize antibodies implicated in multiple sclerosis. The column removes harmful antibodies selectively, leaving all other components of the serum unchanged. The column is used to treat multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                ABP97937-44 represent glycopeptides of a formula given in the specification. The glycopeptides are used to produce columns of the invention. The specification describes immunoabsorption columns,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycopeptide #5 for diagnosis and treatment of multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel glycopeptides comprising a specific tetrapeptide, useful as diagnostic tools for identifying multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 94; DB 6; Length 17; 100.0%; Pred. No. 7e-09; cive 0; Mismatches 0; Indels
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                                                                                                                                                                        Chelli M,
                                                                                                                                                                                                                                                                                               Claim 4; Page 6; 13pp; English.
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                                                                 25-JUL-2002; 2002WO-EP008274.
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                                                                                                  25-JUL-2001; 2001IT-FI000144
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                                                                                                                                                                        Pinto F, Papini AM,
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les 17; Conserv
WO2003009887-A2.
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Modified-site
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                                06-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                      novel peptide used in the treatment of autoimmune disease e.g. multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a peptide used in the treatment of autoimmune disease e.g. multiple sclerosis (MS). More particularly, it concerns a Toell receptor sequence found in some MS patients and methods for its detection. T cell receptors comprise alpha and beta chains, with beta chains comprising the following regions from N-terminus to C-terminus: Vbeta-Dbeta-Dbeta-Dbeta-Dbeta T cell receptors naturally vary in the Vbeta-Dbeta-Dbeta-Dbeta Grown The peptides of the invention are used for treating autoimmune disease e.g multiple sclerosis. The present sequence is a peptide analogue used in the exemplification of the invention
                                                                                Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Ubeta; Dbeta; immunosuppressive; T-cell receptor; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 94; DB 5; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycopeptide; serum; immunoabsorption column; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residue"
                                               Peptide analogue used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a glycopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "glycosylated
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                                                                                                                                                                                                                                                                                                           (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 2; 64pp; English
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              (first entry)
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-454317/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 AA;
                                                                                                                                                                    WO200216434-A1.
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Modified-site
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              10-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                Zhang JZ;
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Length 17; 0; Indels

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The invention discloses a method for inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, comprising administering a composition comprising a peptide analog in combination with a carrier/adjuvant or diluent. The peptide analog comprises at least of amino acids selected from residues 83 to 99 of human myelin basic protein, where it he L-1ysine at position 91, L-arginine at position 97 or L-threonine at position 95, is altered to another amino acid, and one to three L-amino acids selected from valine at position 86 or 87, histidine at position 88, threonine at position 95 or 98, and proline at position or three L-amino acids selected from valine at position 95 or 99, are altered or an amino acid other than the amino acid present in the pative protein at that position or the L-1ysine at position 91 is altered to another amino acid and the N- and/or C-terminal amino acid are altered to another amino acid and the N- and/or C-terminal amino acids and one to four additional altered residues. The N-terminal amino acids and one to four additional altered residues. The N-terminal amino acids and one to four additional altered residues. The N-terminal additional L-amino acids selected from residues 81 to 90 and 92 to 99 is substituted with a charged amino acid. The method is useful for treating multiple sclerosis using peptide analogs of human myelin basic protein. The sequence presented is the wild-type human myelin basic protein. The sequence presented is the wild-type human myelin basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, useful for treating multiple sclerosis, comprises administering an amount of a pharmaceutical composition comprising a
basic protein minimal epitope which can be used in a fusion protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, Th2; immune response; myelin basic protein; peptide analog;
proteolysis; multiple sclerosis; neuroprotective; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wild-type human myelin basic protein peptide analog.
                                                                                                                           Score 94; DB 6;
Pred. No. 7e-09;
                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 3; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NEUR-) NEUROCRINE BIOSCIENCES INC.
                                                                                                      100.0%; Sc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                   ADE50773 standard; peptide; 17 AA.
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98US-00137759.
99US-00378244.
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                                                                                                                                                                                    17; Conservative
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                                                                                                                              Query Match
Best Local Similarity
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                                                                             Sequence 17 AA;
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                             the invention
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                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                       ö
                                                   The present invention relates to glycopeptides (ABR56059-ABR56066). The glycopeptides have high specificity in recognizing autoantibodies involved in multiple sclerosis pathology, and thus are effectively used in diagnosis and treatment for multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising polypeptide sequences that bind to IgG
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                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                    100.0%; Score 94; DB 6; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human myelin basic protein MBP minimal epitope.
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        Claim 7; Page 12; 14pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-103456/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases.
                                                                                                                                                                                                                                                          Best Local Similarity
Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang K,
                                                                                                                                                                                      Sequence 17 AA;
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Homo sapiens.

AA019672;

RESULT 7 AA019672

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Query Match

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having an isolated, prepared epitope selected from any of the sequences

from 30 lists given in the specification. Also disclosed is a method for

inducing a cytotoxic T cell response against a pre-selected antigen in a

c patient expressing a specific MHC class I allele by contacting cytotoxic

composition comprises an epitope that is joined by an amino acid linker.

C composition comprises an epitope that is joined by an amino acid linker.

The epitope is admixed or joined to a CTL or HTL epitope. The epitope is

bound to an HLA molecule on the antigen-presenting cell, where when an A2

creatricted cytotoxic Imphocyte (CTL) is present, a receptor of the CTL

binds to a complex of the HLA molecule and the epitope. Specifically

claimed are peptides having allele-specific binding motifs for HLA. The

compositions and methods are useful for preventing, treating or

ciamed agents for evaluating immune responses, for making antibodies

diagnostic agents for evaluating immune responses, for making antibodies

and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virucide, cytostatic, gene therapy, vaccine, epitope, cytotoxic T cell, MHC class I, CTL, HTL, A2-restricted cytotoxic lymphocyte, HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
                                                                                                                                                                   Gaps
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                                                                                            Score 94; DB 7; Length 17;
Pred. No. 7e-09;
); Mismatches 0; Indels
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100.0%; Score 94; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                            100.0%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADW36476 standard; peptide; 17 AA.
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                                                                                                                                                                                                                                                                  1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                               1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2001; 2001WO-US051650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA binding epitope #7226
                                                                                                                            Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral disease; cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-441519/41
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                            Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADW36476;
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                                                                                            Query Match
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having an isolated, prepared epitopes selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigon in a patient expressing a specific MFC class I allele by contacting cytotoxic composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a TL or HTL epitope. The epitope is bound to an HLA molecule and the epitope. The epitope is bound to an HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnosing viral diseases and cancer. The peptide epitopes are useful as and for evaluating efficacy of a vaccine. Sequences given in AbW3251-ADW3775 represent epitopes of the invention as given in Tables 2-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell; MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA; viral disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a composition comprising at least one peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 52-379; 382pp; English.
                                                                                                                                                                                                                      ADW35045 standard; peptide; 17 AA.
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17
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                                    1 ENPVVHFFKNIVTPRTP
                                                                                                                                                                                                                                                                                                                                                   10-MAR-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               HLA binding epitope #5795
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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RESULT 11 ADW33812

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Human; myelin basic protein; vaccine; multiple sclerosis; T cell.
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                                                                                                              06-AUG-2003; 2003WO-US024548.
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                                                                                                                                                                                                                                WPI; 2004-180654/17.
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                                                            WO2004015070-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 AA;
                                    Homo sapiens.
                                                                                     19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                      Zhang JZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL18291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL1829:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytocoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is from tha molecule on the antigon-presenting cell, where when an A2-restricted cytocoxic lymphocyte (CTL) is present; a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnosing viral diseases and cancer. The peptide epitopes are useful as and for evaluating efficacy of a vaccine. Sequences given in ADW29221.

ADW37745 represent epitopes of the invention as given in Tables 2-31.
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                                                                                                  Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell; MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
                                                                                                                                                                                                                                                                                                                                                                       New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human myelin basic protein peptide fragment MBP-1 (aal10-126).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 94; DB 7; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 52-379; 382pp; English.
ADW33812 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK67704 standard; peptide; 17 AA.
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                                                                                                                                                                                                                                 18-OCT-2001; 2001WO-US051650.
                                                                                                                                                                                                                                                         19-OCT-2000; 2000US-0242350P.
20-APR-2001; 2001US-0285624P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                (first entry)
                                                                          HLA binding epitope #4562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                MHC class I; CTL; HTL viral disease; cancer
                                                                                                                                                                                                                                                                                                 (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                        Sidney J,
                                                                                                                                                                                                                                                                                                                                                WPI; 2003-441519/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 AA;
                                                                                                                                                    Unidentified.
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                                                10-MAR-2005
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                        ADW33812;
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The present invention is direct to methods of isolating antigen specific comprises inclubating a sample of T cells obtained from a patient with the comprises inclubating a sample of T cells obtained from a patient with the antigen and selecting T cells that express one or more of first markers cantigen and selecting T cells that express one or more of first markers cantigen and selecting T cells that express one or more second markers selected from interleukin-2, interferongamma, tumour necrosis factor alpha, interleukin-2, interferongamma, tumour necrosis can the pathogenesis of autoimmune diseases. The methods also permit the disease and for monitoring the efficacy of treatment. The methods are preparation of autologous T cells which play a role the disease and for monitoring the efficacy of treatment. The methods also paration of autologous T cell vaccines for the treatment of the disease and for monitoring the proparation of autoimmune diseases. The monitoring the progression of the proparation of antigen-specific T cells optionally followed by culturing steps which allow the expansion of the population of solation of myelin-reactive T cells optionally followed by culturing specific T cells and expansion of the population of solation of myelin-reactive T cells for T cell vaccination. Peripheral blood of myelin-reactive T cells from the invention describes the isolation of patients and incubated with peptides comprising known immunodominant creamine and anno acide 110-126 of human myelin basic protein. Cells were comprises amino acide 110-126 of human myelin basic protein. The compositions of the invention are useful for the diagnosis cand/or treatment of autoimmune thyeaces es propagated in culture. The methods and compositions of the invention are useful for the diagnosis cand/or treatment of autoimmune thyeaces or T cell associated conditions of extrement and probated and promise and confined and charmance of autoimmune thyeins, specials is gisease, inflammatory human to be extremed to a propagated in cul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                    Isolating one or more T cells specific for an antigen of interest comprises incubating a T cell sample with an antigen, useful for diagnosing or treating multiple sclerosis, psoriasis, thyroiditie, diabetes and rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erythematosus, autoimmune thyroiditis, Grave's di
bowel disease, diabetes and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 1; 38pp; English.
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(BAYU ) BAYLOR COLLEGE MEDICINE. (OPEX-) OPEXA PHARM INC.
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The invention comprises a method of determining etiology of an autistic spectrum disorder in a patient. The method involves determining the level of an infectious agent, toxic chemical, or dietary protein derived antigen, or their antibodies in samples of patient, and comparing antigens/antibodies levels with normal levels of antigens/antibodies from control subjects. The method of the invention is useful for determining the etiology of an autistic spectrum disorder, such as autism, pervasive development disorder and Asperger's syndrome. The present amino acid sequence represents a peptide that was used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                          Determining etiology of autistic spectrum disorder in patient, by determining level of infectious agent/toxic chemical/dietary protein derived antigen in samples of patient, comparing it with normal level of antigens of control subjects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical; t-lymphocyte; antigen; multiple sclerosis; utcimmune disease; immunety; immune stimulation; immunity; autcoimmunity; immunosuppressiv; neuroprotective; antiarthritic; antirheumatic; antiinfalfammatory; myelin; myelin basic protein; MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 94; DB 9; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myelin basic protein (MBP) peptide, amino acids 83-99.
    autism; nootropic; asperger syndrome; MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 6; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEB86495 standard; peptide; 17 AA.
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                                                                                                                                                                                          03-FEB-2004; 2004US-00770712.
                                                                                                                                                                                                                                         03-FEB-2004; 2004US-00770712.
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                                                                                                                                                                                                                                                                                   (VOJD/) VOJDANI A.
                                                                                                  US2005170333-A1
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                                                                                                                                                                                                                                                                                                                                  Vojdani A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method of diagnosing the likelihood and severity of demyelinating diseases. The method involves determining antibodies against neuron-specific antigen in sample, comparing the level of antibodies with the normal level of antibodies, where normal level of antibodies for heuron-specific antigen indicate optimal conditions, lower than or higher than normal level of antibodies for the antigen indicate of an absence of or a likelihood of demyelinating diseases, respectively.

The neuron-specific antigen is chosen from myelin basic protein (MBP), myelin oligodendrocyte glycoprotein, myelin ossociated glycoprotein, transaldolase, glial fibrillary protein, S-100 protein, cross-reactive peptide from dietary protein, cross-reactive peptide from dietary protein, cross-reactive peptide from dietary protein, and phosphodiesterase. The immunoassay is an enzyme linked immunosorbent assay (ELISA) test. The method is useful for diagnosing the likelihood and severity of demyelinating diseases such as multiple sclerosis in a patient. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing likelihood and severity of demyelinating disease, by determining antibodies against neuron-specific antigen, comparing level of detected antibodies with normal level for detecting absence/likelihood
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                                                                                          Demyelinating disease; neuron-specific antigen; human; myelin basic protein; MBP; myelin oligodendrocyte glycoprotein; myelin basociated glycoprotein; MAG; proteolipid protein; PLP; small heat shock protein; transaldolase; glial fibrillary protein; S-100 protein; cross-reactive peptide; glutamate receptor; phosphodiesterase; multiple sclerosis.
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Pred. No. 7e-09;
Mismatches 0; Indels
                                              Human myelin basic protein (MBP), peptide #2.
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Matches 17; Conservative 0;
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Vojdani A;

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AEB77584;

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RESULT 14 AEB77584

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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Houghten RA, Pinilla C, Martin R, Sturzebecher C; Shukaliak-Quandt J, Mcfarland HF;

WPI; 2005-555771/56.

Complex peptide mixture having immunomodulatory effects, useful for preparing medicament for treating autoimmune disease e.g. multiple sclerosis, rheumatoid arthritis, for preparing medicament for stimulating immune cell.

Example; Page 22; 51pp; English

The invention relates to complex peptide mixtures comprises several peptides having 8-20 amino acids, where the mixture comprises peptides having 8-20 amino acids, where the mixture comprises peptides having a degree of diversity at defined positions in the peptide chain, where the degree of diversity in the defined position is different from other defined positions, and where in the majority of the mixture, the peptides includes Ala, Glu, Lys and Tyr and no other amino acids, in at least four positions. Also described are: (1) a method of creating a high affinity peptide ligand of a defined formula for a receptor of a T cell that is reactive to a myelin antigen, copolyamer, or an active mixture; and (2) a method of enhancing a biological property of a complex mixture of peptide mixture is useful in the preparation of a madicament for treating a disease such as multiple sclerosis (8S) and experimental autoimmune encephalomyelitis (EAE). It is also useful for preparing a medicament for stimulating an immune cell, or for suppression of an immune reaction (e.g. autoimmune reaction) to an antigen derived from myelin. This sequence represents a myelin peptide used in the examples of the present invention.

Sequence 17 AA;

Gaps ö 100.0%; Score 94; DB 9; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels Local Similarity 100.0 Query Match Best Loca Matches

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1 ENPVVHFFKNIVTPRTP 17 ENPVOHEFKNIVTPRTP 17 ò g

Search completed: February 22, 2006, 21:30:49
Job time : 14.1572 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OGGMW7 HUMAN
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Maximum Match 100%
Listing first 45 summaries
                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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11D TGGGGG HIGHOUN STANDARD; PRT; 330 AA.

AC POISST: HIGHOUN STANDARD; PRT; 330 AA.

AC POISST: GRILL 101, Created)

DE 1.JUL-1986 (Rel. 01, Created)

1.JUL-1986 (Rel. 01, Last sequence update)

1.JUL-1986 (Rel. 01, Last sequence update)

2.JUL-1986 (Rel. 01, Last sequence update)

1.JUL-1986 (Rel. 01, Last sequence update)

1.JUL-1986 (Rel. 01, Last sequence update)

2.JUL-1986 (Rel. 01, Last sequence update)

3.JUL-1986 (Rel. 01, Lel. 01, Rel. 01,
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K -> R (in GlM(3) marker).
/FIId=VAR 003886.
D -> E (in GlM(non-1) marker).
FIId=VAR 003887.
L -> M (in GlM(non-1) marker).
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Pred. No. 5.9e-90;
3; Mismatches 4;
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                                                                               MEDLINE=7707026'; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Breker L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (upseloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
            Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulface bonds ";
Blochemistry 9:3188-3196(1970).
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GO; GO:0003825; F:antigen binding; TAS.
GO; GO:0006855; P:immune response; NAS.
InterPro; IPR00710: Ig-like.
InterPro; IPR0031006; Ig_MHC.
Pfam; PPO7654; CI-set; J.
PROSITE; PS00290; IG_MHC; 2.
3D-structure; Direct protein sequencing; Glycoprotein; Immunoglobulin C region; Immunoglobulin C region; Immunoglobulin G region; Immunoglobulin G region; Immunoglobulin domain.
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  MEDLINE=71064027; PubMed=4923144;
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PDB; IAA7; X-ray; H=1-103.
PDB; ID58; X-ray; H=1-101.
PDB; ID59; X-ray; H=1-101.
PDB; ID69; X-ray; H=1-101.
PDB; ID60; X-ray; H=1-101.
PDB; ID60; X-ray; H=1-101.
PDB; IEA4; X-ray; A/B=106-329.
PDB; IFC2; X-ray; A/B=106-329.
PDB; IFC2; X-ray; A/B=106-329.
PDB; ITC3; X-ray; A/B=107-330.
PDB; IIX; X-ray; A/B=107-330.
PDB; IIX; X-ray; A/B=107-330.
PDB; IIX; X-ray; A/B=107-330.
PDB; IIX; X-ray; A/B=107-330.
PDB; ITX; X-ray; A/B=107-330.
PDB; ITX; X-ray; A/B=107-330.
PDB; ITX; X-ray; A/B=107-330.
PDB; IC60; X-ray; A/B=107-330.
PDB; A/B=106-326.
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9 1 BPKSCDKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF

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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Fedingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Diatchenko L., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Prapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
                                                       159 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
                                                                                           121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                            219 ISKAKGQPREPQVYTLPPSRDELIKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTIP
                                        NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                279 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 465 AA, 51083 MW, B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                        GGGWK6;

GJ-JUL-2004 (TrEMBLrel. 27, Created)

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Hypothetical protein.

Homo sapiens (Human).
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GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN_2.
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InterPro; IPR007110; IG-like.
InterPro; IPR003109; IG cl.
InterPro; IPR003506; IG cl.
InterPro; IPR003506; IG will
Efam; PP07654; Cl-set; 3.
SWART; SW00409; IG; 2.
SWART; SW00407; IGcl; 3.
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feathgold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Antschako L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P. H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muany D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A. Miland D.K., Schein J.E., Jones S.J.M., Marra M.A.;
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A. Manna M. Anilaia I. analysis of more than 15,000 full-length human
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                             NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                             ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                    EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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       Length 465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                               4,
   97.2%; Score 1225; DB 2; 97.0%; Pred. No. 9.1e-90; ive 3; Mismatches 4;
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INCEPTO; IPR001559; IG.
INCEPTO; IPR001597; IG-11.
INCEPTO; IPR003597; IG-11.
INCEPTO; IPR003597; IG-11.
INCEPTO; IPR003597; IG-11.
INCEPTO; IPR003596; IG-11.
INCEPTO; IPR003596; IG-11.
Pfam; PF07654; C1-8et; 3.
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Query Match
Best Local Similarity 97.0°
Matches 225; Conservative
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Name=IGHG1;
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Query Match
Best Local Similarity 97.0<sup>3</sup>
Matches 225; Conservative
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Q7Z7PS;
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01-0CT-2003 (TFEMBLrel. 2.
01-MRR-2004 (TFEMBLrel. 21
IGHG1 protein.
Name=IGHG1;
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Klausherg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Bask S.A., McKwan P.J., McKernan K.J., Malk J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garrinci P., Gunzarne P.H.,

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Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                      1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                       61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 PVLDSDGSFFLYSKITVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                   Score 1225; DB 2; Length 466;
Pred. No. 9.1e-90;
3; Mismatches 4; Indels
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EMBL, BC092518; AAH92518.1; -; mRNA.
SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
                       SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS500295; IG_MIC; 4.
PROSITE; PS500290; IG_MHC; UNKNOWN 2.
SEQUENCE 466 AA; 50854 MW; 53EB0BCEDEB1076E CRC64;
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Last annotation update)
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SMART; SM00409; IG; 2.
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TISSUE-Spleen,
WEDLINE-2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marushas K., Farmer A.A., Rubin G.M., Heiseh F.,
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A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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A Hakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C. Garning M.A., Schein J.E., Jones S.J.M., Marra M.A.;
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C. Garning M.A., Schein J.E., Jones S.J.M., Marra M.A.;
C. Garning M.A., Schein J.E., Jones C. M.A., Marra M.A.;
C. Garning M.A., Schein J.E., Jones C. M.A., Sadatha M.A.;
C. Garning M.A., Schein J.E., Jones C. M.A., Marra M.A.;
C. Garning M.A., Schein J.E., Jones C. M.A., Marra M.A.;
C. Garning M.A., Schein J.E., Jones C. M.A., Marra M.A.;
C. Garning M.A., Schein J.E
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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     Length 469;
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97.2%; Score 1225; DB 2;
97.0%; Pred. No. 9.2e-90;
iive 3; Mismatches 4;
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EMBL, BCO51328, AAH51328.1; -; mRNA.
HSSP, PU1857; 1HZH.
SWR, Q727P5; 20-469.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig WHC.
InterPro; IPR003066; Ig WHC.
InterPro; IPR003596; Ig Y.
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Yilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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A Hakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Salska U., Salska D.E.,
Schnerch A., Schin J.B., Jones S.J.M., Marra M.A.,
Schnerch A., Schin J.B., Jones S.J.M., Marra M.A.,
                                                                                                                                                      NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                    1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                            PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                              PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                             Query Match 97.2%; Score 1225; DB 2; Length 469; Best Local Similarity 97.0%; Pred. No. 9.2e-90; Matches 225; Conservative 3; Mismatches 4; Indels (
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO53984; AAH53984.1; -; mRNA.
HSSP; P01857; 1HZH.
                                                        51395 MW; C8DSBE12BAAF795C CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                          470 AA
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00299; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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InterPro; IPR003597; Ig_c1.
                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2003 (TrEMBLrel. 25, 01-0MR-2004 (TrEMBLrel. 26, 14) MRA-2004 (TrEMBLrel. 26, Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                        Q7Z5W1 HUMAN PRELIMINARY;
Q7Z5W1;
                                       Immunoglobulin domain.
SEQUENCE 469 AA; 51
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TISSUE-Primary B-Cells;

WEDINE-238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

Krausberg R.D., Felingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                    Length 470;
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TISSUB-Primary B-Cells;
NIH MGC Project;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF07654; Cl_set; 3.

SMART; SM0406; IGv. 1.

PROSITE; PS00290; IG_MIKE; 4.

PROSITE; PS00290; IG_MIKE; MRC: UNKNOWN 2.

Hypochetical protein; Immunoqlobulin domain.

SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                             Score 1225; DB 2;
Pred. No. 9.2e-90;
                                                                                                                                                                                                                                                                                        97.2%; Scur.
97.0%; Pred. No. >...
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    225; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                            61 NWYDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                            Length 472;
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                                                                                           Indels
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
110-MAY-2005 (TrEMBLrel. 30, Last senteation update)
Anti-RhD monoclonal T125 gammal heavy chain precursor.
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97.0%; Pred. No. 9.3e-90;
ilve 3; Mismatches 4;
                        Score 1225; DB 2;
Pred. No. 9.2e-90;
   97.2%; Scor.
97.0%; Pred. No. 5...
3; Mismatches
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                                                        Best Local Similarity 97.0
Matches 225; Conservative
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                               Query Match
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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A Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
EMBL; BX640627; CR45781.1; -; mRNA.
HSSP; P01861; 1ADQ.
R InterPro; IPR001399; Ig.
R InterPro; IPR001399; Ig.
R InterPro; IPR001399; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R R RPR0515; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGV; 1.
R PROSITE; PS00835; IG_LIKE; 4.
R PROSITE; PS00835; IG_LIKE; 4.
R PROSITE; PS00835; IG_LIKE; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 97.2%; Score 1225; DB 2; Length 470; Local Similarity 97.0%; Pred. No. 9.2e-90; neg 225; Conservative 3; Mismatches 4; Indels (
                                                        SMR; GGEDAA; 20-470.

**InterPro; IPR003599; Ig.

**InterPro; IPR003006; Ig_MC.

**InterPro; IPR003006; Ig_MC.

**InterPro; IPR003006; Ig_MC.

**InterPro; IPR003596; Ig_V.

**InterPro; IPR003596; Ig_V.

**InterPro; IPR003596; Ig_V.

**SMART; SM00409; IG; 2.

**SMART; SM00409; IG; 3.

**SMART; SM00409; IG; 1.

**SMART; SM00409; I
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686F15220.
Name=DKFZp686F15220;
BC018747; AAH18747.1; -; mRNA.
P01861; 1ADQ.
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TISSUE=Rectum tumor;
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MEDLINE-229825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-229825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetew K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetew K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jeeberg B., Buetew K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Racheley R.W., Touchman J.W., Garen B.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                             ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                   304 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                 364 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                   NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                    424 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 475
                                                                                                                                                                                                                                                               PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; EC073773; AAH73773.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGGMX1_HUMAN PRELIMINARY;
QGGMX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
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244 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVUDVSHEDPEVKF 303
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073782; AAH73782.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
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                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                       475 AA
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
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InterPro; IPR007110; IG-11ke.
InterPro; IPR007110; Ig-21.
InterPro; IPR003596; Ig.MHC.
InterPro; IPR003596; Ig.MHC.
InterPro; IPR003596; Ig.MHC.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
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                                                                                                                                                                                                                                                                                    QGGMW7_HUMAN PRELIMINARY;
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SEQUENCE 475 AA;
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TISSUE=Spleen;
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HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEP055_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                    Matches 225; Conservative
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Best Local Similarity
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                                                                                    120
                                                                                                           364
                                                                                                                                                            424
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"Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
                                                                                                                                                                                                                                                                                                                                                            Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                     61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                 365 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                    1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
              Gaps
                                                                                                                                                                                    PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                  PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 476
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MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hu Z., Garen Ā.;
Submitted (FRB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF272774; AAK58686.2; -; mENA.
HSSP; P08709; 1KLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ensembl; ENSG0000057593; Homo sapiens.

G0; G0:0005576; C:extracellular region; IEA.

G0; G0:0005509; F:calcium ion binding; IEA.

G0; G0:0004263; F:chymotrypsin activity; IEA.

G0; G0:0004263; F:rypsin activity; IEA.

G0; G0:0006509; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000152; Asx_hydroxyl_S.
                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
Factor VII active site mutant immunoconjugate.
Homo sapiens (Human)
 Pred. No. 9.3e-90; 3; Mismatches 4
                                                                                                                                                                                                                                                                         679 AA
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InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF07654; C1-set; 2.
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InterPro; IPR001481; BGF_Ca.
InterPro; IPR001439; BGF_Ike.
InterPro; IPR005209; BGF_Ike.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001710; Igg-Ike.
InterPro; IPR003597; Ig-Ike.
InterPro; IPR003597; Ig-Ike.
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PRINTS; PR00122; GHYMOTRYPSIN.
PRINTS; PR00101; GEPBLOOD.
PRINTS; PR00001; GLABLOOD.
97.0%;
                                                                                                                                                                                                                                                                      Q96PQ8_HUMAN PRELIMINARY;
Q96PQ8;
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           Matches 225; Conservative
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 Local Similarity
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PROLEGOIDE SEQUENCE.

TISSUE-PETIPHERAIN Nervous System;

TISSUE-PETIPHERAIN Nervous System;

A Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

Ratusherg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

Ratusherg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

Ratusherg R.L., Feligold E.A., Grouse L.H., Schwler G.D.,

A lighting R.F., Jordan H., Moore T., Mars S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Toshiyaki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.R., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley A., Young A.C., Shevchenko Y., Bouffard G.G.,

Nilling M., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Rochert A., Schein J.E., Jones S.J.M., Marka M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568 ISKAKGQPREPQVYILPPSKDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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Last annotation update)
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Pred. No. 1.5e-89;
SMART; SMUODO2; ....;
SMART; SMUODO2; ....;
SMART; SMOODO2; TYP_SPC; 1.
PROSITE; PSOODO2; EGF 1; UNKNOWN_1.
PROSITE; PSOODO2; EGF 2; 1.
PROSITE; PSOODO2; EGF 2; 1.
PROSITE; PSOODO3; EGF 2; 1.
PROSITE; PSOODO1; EGF 2; 1.
PROSITE; PSOODO1; EGF 2; 1.
PROSITE; PSOODO1; EGF 2; 1.
PROSITE; PSOODO3; EGF 2; 1.
PROSITE; PSOODO39; EGF 2; 1.
PROSITE; PSOODO39; EGF 2; 1.
PROSITE; PSOODO30; ERYPSIN_HIS; UNKNOWN_1.
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244 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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The German cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger .
Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640622; CAE45776.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEGLHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                    Length 475;
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                                                                                                                                                                                                                                                                                                     5; Indels
                         SWART; SM00409; IG; 2.
SWART; SM00409; IGG1, 3.
SWART; SM00400; IGG1, 3.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypochhetical protein.
SEQUENCE 475 A4; 52043 MW; B7EAE255A26F4B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein SEQUENCE 480 AA: 52612 MW; 225247F3D35AEC18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686001196.
Name=DKFZp686001196;
Homo sapiens (Human)
                                                                                                                                                                                                                                           Query Match 96.9%; Score 1221; DB 2; Best Local Similarity 96.6%; Pred. No. 1.9e-89; Matches 224; Conservative 3; Mismatches 5;
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003596; Ig_V.
Pfam; PPF00564; C1-set; 3.
SWART; SW00409; IG; 2.
SWART; SW00407; IGC1; 3.
SWART; SW00407; IGC1; 3.
PROSITE; PS00290; IG_LKE; 4.
PROSITE; PS00290; IG_LKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGN094 HUMAN PRELIMINARY;
Q6N094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 224; Conservative
  Pfam; PF07654; C1-set; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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TISSUB-Esophagus tumor;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo (Han M., Wiemann S.;
Submitted (JMN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640947; CAE45972.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                                                 TISSUE-Peripheral Nervous System;

A Strausberg R.;
Strausberg R.;
Submit of JAN-2014) to the EMBL/GenBank/DDBJ databases.

R Submit BCG6520, AA465820.1; -; mRNA.

R HSSP; P01861; 1ADQ.

R InterPro; IPR001359; Ig.

R InterPro; IPR003109; Ig.

R InterPro; IPR003109; Ig.

R InterPro; IPR003597; Ig.

R InterPro; IPR003597; Ig.

R InterPro; IPR003597; Ig.

R SMART; SMO0409; Ig. 2.

R SMART; SMO0409; IG. 1.

R PROSITE; PS00299; IG. MKC, WHYPOCHELICAL PROCEIN.

HYPOCHELICAL PROCES.

SEQUENCE 473 AA; S1344 MW; 9816D56A77129B57 CRC64;
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QGMZQG_
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein DKFZp686G11190.
Name=DKFZp686G11190;
                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
96.9%; Score 1221; DB 2;
Best Local Similarity 96.6%; Pred. No. 1.9e-89;
Matches 224; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3, Mismatches
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InterPro; IPR003599; Ig.
InterPro; IPR003110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_WHC.
mouse cDNA sequences.";
                                                                                NUCLEOTIDE SEQUENCE
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249 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKF 308
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> Sequence 14 Sequence 16 Sequence 18 Sequence 65 Sequence 14

Sequence 18 Sequence 2, Sequence 2, Sequence 14

Sequence 8, A Sequence 8, A Sequence 7, A Sequence 4, A Sequence 25, Sequence 25,

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COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER. IBM PC compatible OPERATING SYSTEM:
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/84277
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/124329
FILING DATE: 02-OCT-1987
ATTORNEY ABRICATION NUMBER: 07/104329
FILING DATE: 1906-DETER DATES DETER DATES DATES DATES DATES DATES DETER DATES DATES
US-09-526-098-8
US-09-383-916-8
US-09-756-424-8
US-09-776-424-8
US-09-738-741-4
US-09-740-002-25
US-09-301-593-22
US-08-887-3528-14
US-08-887-3528-16
US-08-109-207C-14
US-09-109-207C-14
US-09-109-207C-18
                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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TELECOMMUNICATION INFORMATION:
TELEFHONE: 415/252-1896
TELEFAX: 415/952-981
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTRRISTICS:
LENGTH: 371 amino acids
TYPE: amino acids
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 RESULT 1
US-08-236-311-7
 1725
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   Sequence 3730, Ap
Sequence 10, Appl
Sequence 54, Appl
Sequence 16, Appl
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16, Appl
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Sequence 41, Appl
Sequence 42, Appl
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                                                                                                               February 22, 2006, 21:37:34; Search time 49.0155 Seconds (without alignments) 556.619 Million cell updates/sec
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                   GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/FCOMB.pep:*

(cgn2_6/ptodata/1/iaa/FCOMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-458-516-13
US-08-030-175-42
US-08-030-175-42
US-08-30-175-42
US-08-376-359A-54
US-09-825-561A-16
US-09-825-561A-16
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US-09-825-561A-16
US-09-825-561A-16
US-09-825-61A-7
US-09-848-550-12
US-09-848-550-12
US-09-848-550-12
US-09-526-098-4
US-09-526-098-4
US-09-526-098-12
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                                                                                                                                                                                                                                                                                                            572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1764
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Match Length
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PSVPLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSVGSFFLYSKLIVDKSRW 300
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                                                                                                                                                                                                                                                                                                                                                                             42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPBFPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                     Length 371;
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER: READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: DATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,408
FILING DATE: 28-May-2002
FILING DATE: 28-May-2002
FILING DATE: 1-UNN-1995
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-UNN-1995
APPLICATION NUMBER: 07/936190
                                                                                                                                                                                                                                                                   Score 1729; DB 2;
Pred. No. 1.1e-156;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-10-157-408-7
Sequence 7, Application US/10157408
Patent No. 6710169
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 OCGNVFSCSVMHEALHNHYOORSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 QQGNVFSCSVMHRALHNHYTQKSLSLSPGK 371
                 P0444P1C3
             REFERENCE/DOCKET NUMBER: P044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-981
TELEFAX: 415/952-981
TELEY: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        98.0%;
                                                                                                                                                                LENGTH: 371 amino acids

1 TYPE: amino acid

1 TOPOLOGY: linear

US-08-457-918-7
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.9
Matches 323; Conservative
REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                              PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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                                                                                     Gaps
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                                   Length 371;
                                                                                 4; Indels
                                     Score 1729; DB 1;
Pred. No. 1.1e-156;
3; Mismatches 4;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: patin (Generation)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-UNN-1995
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/236311
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/84277
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION NUMBER: 07/104329
PRIOR APPLICATION NUMBER: 07/104329
PRIORNEY/AGENT INPORMATION:
                                         98.0%;
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                                     Query Match
Best Local Similarity 97.9'
Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-457-918-7
  US-08-236-311-7
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117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Milliam M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
     OPERATING SYSTEM: PC_DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.0%; Score 1729; DB 2; Best Local Similarity 97.9%; Pred. No. 1.5e-156; Matches 323; Conservative 3; Mismatches 4;
                                                                                                                                                 PRIOR APPLICATION: Act
PRIOR APPLICATION: Act
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-ARR-1992
FILING DATE: 27-ARR-1992
ATORNEY AGENT INFORMATION:
NAME: Smith, William M.
REFERENCE FOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STREE mino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-397-411-7
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                                                                                                             FILING DATE: 01 CLASSIFICATION:
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US-08-458-516-13
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APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STRRET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STRYE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 371;
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98.0%; Score 1729; DB 2;
Best Local Similarity 97.9%; Pred. No. 1.1e-156;
Matches 323; Conservative 3; Mismatches 4;
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
RFFERENCE/DOCKET WUMBER: P0444PIC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-198
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 371 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-157-408-7
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181 STYRVVSVLTVIHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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                                                     Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.0%; Score 1729; DB 2; Best Local Similarity 97.9%; Pred. No. 1.6e-156; Matches 323; Conservative 3; Mismatches 4;
     301 OQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acide TOPOLOGY: 14-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-030-175-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-030-175-42
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APPLICANT: Clark, Michael R.
APPLICANT: Clark, Michael R.
APPLICANT: Cobold, Stephen P.
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kuzz, P. C.
STREET: 555 13TH ST., NW Suite 701 East
CITY: Washington
STATE: D. C.
COUNTRY: U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 449;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION NUMBER: US/08/458,516
FILING DATE: 03-MAY-1993
ATYONEY/AGENT INFORMATION:
NAME: SMATH, William REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET WUMBER: 11823-37-3
TELEPPAK: 415-326-2400
TELEPRAX: 415-326-2400
TELEPRAX: 415-326-2400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LEMETHER OF SEQ ID NO: 13:
LE
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Pred. No. 1.5e-156;
3; Mismatches 4;
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US-08-030-175-41
; Sequence 41, Application US/08030175
; Setent No. 6767996
; GENERAL INFORMATION:
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Best Local Similarity 97.9%;
Matches 323; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                    Length 470;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                Query Match 98.0%; Score 1729; DB 2; Best Local Similarity 97.9%; Pred. No. 1.6e-156; Matches 323; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08378939;
Patent No. 5876961;
GENERAL INFORMATION:
APPLICANT: LEWIS, ALAN PETER;
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES;
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ;
STREET: SSS THIRTEBNTH ST. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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amino acid
                                          ; ORGANISM: Homo sapiens
US-10-104-047-3730
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US-08-378-939-10
LENGTH: 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 PSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317
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         COMPUTER READABLE FORM:

MEDIUN TYPE: EN AT Compatible
COMPUTER: ELBA AT Compatible
COMPUTER: ELBA AT Compatible
COMPUTER: ELBA AT Compatible
COMPUTER: WordPerfect 5.0 (Dos Text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175
FILING DATE: 17-MAY-1993
CLASSIFCATION: 424
RRIOR APPLICATION: 424
RRIOR APPLICATION: A24
FRIOR APPLICATION: A24
RAPPLICATION: A24
RAPPLICATION: A24
RRIOR APPLICATION: A24
RRIOR APPLICATION: A24
REFERENCE (DOCKET NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 30,377
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 42:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 467 amino acids
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Patent No. 6943241

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION UNBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acida TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.99
Matches 323; Conservative
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US-10-104-047-3730
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                                                                                                                                                                                        398 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 457
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                                                                                                   338 PSVFLFPPKRKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 397
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                   238 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFFAVLQSS
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                                                                             PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                                               STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 67775394K, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: No. 80LUBLE ZALPHAII CYTOKINE RECEPTORS
TITLE OF INVENTION: SOLUBLE ZALPHAII CYTOKINE RECEPTORS
TITLE OF INVENTION: SOLUBLE ZALPHAII CYTOKINE RECEPTORS
CURRENT APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/122,121
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
TYPE: PRT
CHARLE PRESERVE FASTS OF MAINDOWS ARRIED SEQUENCE
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US-09-825-561A-16
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98.0%; Score 1729; DB 2;
Best Local Similarity 97.9%; Pred. No. 2.1e-156;
Matches 323; Conservative 3; Mismatches 4;
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                                                                               Length 476;
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APPLICANT: Foster, Donald C.
APPLICANT: Xu, wenfeng
APPLICANT: Xu, wenfeng
APPLICANT: Xu, wenfeng
APPLICANT: Xeren L.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Began, Maribeth A.
APPLICANT: Began, Maribeth A.
APPLICANT: Chandragekher, Yasmin A.
APPLICANT: Oc. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
CURRENT APPLICATION NUMBER: 05/011,969
REIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72.
SOFTWARE: FastSEQ for Windows Version 3.0
SEG ID NO 54
                                                                               Score 1729; DB 1;
Pred. No. 1.6e-156;
3; Mismatches 4;
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Matches 323; Conservative
                 , MOLECULE TYPE: protein US-08-378-939-10
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ORGANISM: Homo sapiens
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Best Local Simil
Matches 323; C
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TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING FILLE REFERENCE: REG 203-A CURRENT APPLICATION NUMBER: US/09/313,942 CURRENT FILLING DATE: 1999-05-19 PRIOR PAPLICATION NUMBER: 09/313,942 PRIOR PAPLICATION NUMBER: 60/101,858 PRIOR PILLING DATE: 1998-09-25 NUMBER OF SEQ ID NOS: 32 SOFTWARE: FRANKE: FRANKE
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Sequence 9, Application US/10282162
Patent No. 6927044
Fatent No. 692708
Fatent No. 692708
Fatent Reference: Ref 203-B-US
FATENT APPLICATION NUMBER: US/10/282,162
FATENT FATENT FATENT NUMBER: 09/787,835
FATENT PAPLICATION NUMBER: 09/787,835
FATENT RELING DATE: 1999-09-22
FATENT PAPLICATION NUMBER: 
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Pred. No. 4.6e-156;
3; Mismatches 4;
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Pred. No. 4.6e-156;
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Best Local Similarity 97.9%;
Matches 323; Conservative
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Best Local Similarity 97.9%;
Matches 323; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Foster, Donald C.
APPLICANT: Wanfeng
APPLICANT: Wanfeng
APPLICANT: Wanfeng
APPLICANT: Wanfeng
APPLICANT: Sprecher, Cludy A.
APPLICANT: Sprecher, Cludy A.
APPLICANT: Bagan, Maribeth A.
APPLICANT: Bagan, Maribeth R.
APPLICANT: Gandraeskher, Yasmin A.
APPLICANT: Chandraeskher, Yasmin A.
APPLICANT: No. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 1999-12-231
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR SEQ ID NOS: 72
NUMBER OF SEQ ID NOS: 72
IENGTH: 571
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98.0%; Score 1729; DB 2;
Best Local Similarity 97.9%; Pred. No. 2.1e-156;
Matches 323; Conservative 3; Mismatches 4;
                                                            301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                               538 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567
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                                                                                                                                                                                                                                                                                                                                                          Sequence 53, Application US/09746359A
Patent No. 6610286
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09313942
Patent No. 6472179
GENERAL INFORMATION:
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| Sequence 7, Application US/09289942A
| Patent No. 6482928
| GRNERAL INFORMATION:
| APPLICANT: Pai, Emil F.
| APPLICANT: Chong, Pele
| APPLICANT: Pedyczak, Arthur
| TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
| TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
| CURRENT APPLICATION NUMBER: US/09/289,942A
| CURRENT FILING DATE: 1999-04-13
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 7
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                   622 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
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US-09-289-942A-7
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Db 433 QQGNVFSCSVMHEALHNHYTQKSLSLSFGK 462
Search completed: February 22, 2006, 21:39:48
Job time: 50.0155 secs
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February 22, 2006, 21:24:11; Search time 216.58 Seconds (without alignments) 669.475 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                        OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aao19664 Human IgG	Adz69628 Human IgG	Aab04071 Zcytor 10	Aam47856 Human Ig-	Aae21960 Human dea	Abb81641 Human IgG	Abb05736 Human imm	Abp71856 Human IgG	Aae32915 Human imm	Aae32627 Human imm	Abr82103 Human DR6	Aao31102 Human A2-	Abr55836 Anti-Ang-		Adf11389 Anti-OPGL	_	Adf83605 Cytokine	Adf75001 Human Ig	Anti-	Adm68911 Human IgG	Adr43460 Heavy cha	Adr31605 Human IgG	Ads87909 Anti-IFN-	
SUMMARIES	ΩI	AA019664	ADZ69628	AAB04071	AAM47856	AAE21960	ABB81641	ABB05736	ABP71856	AAE32915	AAE32627	ABR82103	AA031102	ABR55836	AA030893	ADF11389	ADE97351	ADF83605	ADF75001	ADM41537	ADM68911	ADR43460	ADR31605	ADS87909	
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	Query Match	100.0	98.2	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.0	
	Score	1764	1732	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	
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Ads94906 Anti-IFN-	Ads33009 Human IgG	Adt88869 Human IgG	Adt51577 Heavy cha	Adt51581 Heavy cha	Adt51724 Human Hul	Adu68015 Mouse ant	Adw08868 IGF-IR an	Adw86657 Human imm	Adx97894 Human Ig	Adx98273 Human ant	Ady51253 Human IgG	Human	Human	Aea12531 Human IgG		Aea48148 Human IgG	Aeb86186 Amino aci	Aec08181 Heavy cha		Adw07455 Human 1gG
3 ADS94906	3 ADS33009	3 ADT88869	3 ADT51577	3 ADT51581	3 ADT51724	3 ADU68015	9 ADW08868	9 ADW86657	9 ADX97894	9 ADX98273	9 ADY51253	9 ADY58147	9 ADY26687	9 AEA12531	9 AEA25942	9 AEA48148	9 AEB86186	9 AEC08181	3 ADL35095	9 ADW07455
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1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729
25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human; IgG1; immunoglobulin G; immunotherapy; immune disease; Fcepsilon receptor; autoimmune disease; constrant region; heavy chain; antiathmatic; antiallergic; antiinflammatory; dermatological; antiathritic; antirheumatic; antidiabetic; neuroprotective. Human IgG1 heavy chain constant region. AA019664 standard; protein; 330 AA. 01-MAY-2002; 2002WO-US013527. 01-MAY-2001; 2001US-00847208. 24-OCT-2001; 2001US-00000439. (first entry) Saxon A, Zhang K, Zhu D; (REGC) UNIV CALIFORNIA. WO200288317-A2. 28-MAR-2003 Homo sapiens. 07-NOV-2002. AA019664; AA019664

New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

WPI; 2003-103456/09

Claim 64; Fig 2; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (TIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (RepsilonR). Also provided are nuclectide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for

Adn33230 IgG1-CH h

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                     hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgGI
preferably an IgE-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                                                                                                Length 330;
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                                                                                                                                                                                                                                                                                                                   4; DB 6;
4.6e-125;
an IgE-mediated biological response,
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                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                   100.0%; Score 1764; 100.0%; Pred. No. 4.
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14-APR-2004; 2004US-0562627P.
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                                                                                                                                                                                                       heavy chain constant region
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Misc-difference
                                                                                                                                                                                                                                                                Sequence 330 AA;
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Matches 330;
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The invention relates to a modified FC rusion procesn where a least one amino acid residue from the heavy chain constant region selected from residues 250, 314, and 428 (Rabat numbering) is different from that residues 250, 314, and 428 (Rabat numbering) is different from that present in the unmodified Fc-fusion protein. Also included are an FC fusion protein comprising an Fc region substantially identical to that of the corresponding unmodified Fc-fusion protein, a modified for that that of the corresponding unmodified Fc-fusion protein, a modified CC id class antibody fragment (comprising a heavy chain constant region or Fc-region where at least one amino acid residue selected from that present in the unmodified IgG class antibody, an isolated polynucleotide consisting of residues 250, 314, an isolated polynucleotide consisting of residues antibody, an isolated polynucleotide comprising an amino acid sequence at least 90% identical to a sequence selected from ADZ69600-ADZ69656, an isolated polynucleotide comprising an amino acid residue as cited above, and solated polynucleotide comprising an amino acid residue as cited above, and substituting the selected residue (s) with an amino acid different from the resent in the Fc-fusion protein) and a method of producing a substituting the selected residue (s) with an amino acid different from comprising preparing an expression vector comprising a suitable for FCRN/altered serum half-life as compared with the unmodified Fc-fusion protein with an allow of the compared host cells to produce the modified in the Fc-fusion protein are least of the following protein (comprising preparing an expression vector comprising protein (compared host cells to produce the modified IgG Fc fusion from a tyle 8.0. The fusion proteins are useful for studying protein function in vitro and in vivo and as a potential therapeutic and disponent residue from that is mutated is covered in the feature relature for any than anino acid substitution at residue 250, 314 or 428 (Kabat rangoments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                            New modified Fc-fusion protein where at least one amino acid residue from
the heavy chain constant region, useful for studying protein function in
vitro and in vivo and as potential therapeutic and diagnostic agents.
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                                                                                                                                                                                                 invention relates to a modified Fc-fusion protein where at least
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Best Local Similarity 98.2%; Pred. No. 1.2e-122;
Matches 324; Conservative 2; Mismatches 4;
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                                                                                                                                                     Claim 21; SEQ ID NO 29; 170pp; English
                   WPI; 2005-315683/32
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Isolating a nucleotide which encodes the zcytor 10 cytokine receptor enables the production of recombinant cells expressing the receptor. Those cells can then be used to detect the presence of a medulator of zcytor10 protein by culturing the cells in the presence of a test ligand and comparing levels of activity of mouse zcytor10 in the presence and absence of the test sample. Similarly, detection of zcytor10 receptor ligand within a test sample can be achieved. The method comprising contacting a test sample can be achieved. The method comprising contacting a test sample can be achieved. The method comprising contacting a test sample can be achieved. The method comprising contacting of the zcytor 10 cytokine receptor and detecting the binding of the polypeptide to a ligand in the sample. Specified peptide fragments of the zcytor 10 cytokine receptor and the methods described are used to identify ligands that stimulate the proliferation and/or development of haematopoletic, lymphoid and myeloid cells. Peptide fragments of the cytokine receptor are useful for treating lymphoid, immune, inflammatory, splenic, blood or bone disorders and for generating artibodise directed against the receptor. A vector appressing a secreted human zcytor 10 heterodimer is constructed. In this construct the cytokine binding domain of zcytor 10 is fused to the heavy cytokine receptor and the extracellular portion of the the the heterometric contactor and interior and interi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cytokine receptor mouse zcytor 10, useful for detecting ligands that stimulate proliferation or development of hematopoietic, lymphoid and myeloid cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine receptor subunit (an interleukin receptor subunit) is fused to human kappa light chain (See GENESEQ record AAAS4474). The two sequences are fused together using two primers (AAA54475, AAA54476)
                                                                                                                                                                                                                                                                   zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
binding; detection; modulation; recombinant cell; haematopoietic cell;
lymphoid cell; myeloid cell; lymph; immune system; blood; bone;
inflammatory response; inflammation; spleen; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.0%; Score 1729; DB 4; Length 330; ilarity 97.9%; Pred. No. 2e-122; Conservative 3; Mismatches 4; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presnell SR, Foster DC, Hammond AK,
                                                                                                                                                                                                                  Zcytor 10::IgG gamma fusion peptide.
                                              AAB04071 standard; protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-2000; 2000WO-US012924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00309861.
                                                                                                                                                        11-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-016096/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA54473
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                       AAB04071;
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RESULT 3
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The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding relass of viral RNA and formation of empty capaids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J
                                                                                                                                                                                                LTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
                                                                                                                                                                                                                     Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVBPKSCDKTHTCPPCPAPELLGG
                                                                       121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEGYN
                                                                                                                                            PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                         STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Ig-gammal heavy chain constant region amino acid sequence.
                                                                                                                                                                                                                                                                         301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                              301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                        AAM47856 standard; protein; 330 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-2000; 2000US-0200298P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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N-PSDB; ABA05265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgenic plant.
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ID AAM4
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Best Local Similarity Matches 323; Conserv

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WPI; 2002-351283/38.
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                                                                                                                                                                                                                                                                                                                                                       Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
                                                                                                                                                                             9
chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than animal call culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to
                                                                                                                                                    1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                   GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                   GLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                                                                                                                                                PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREGYN
                                                                                                                                                                                                                                                                                              STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                    STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                           LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human death domain containing receptor (DR6) protein-related protein.
                                                                                                                                 Gaps
                                                                                                                                ;
                                                                                                       Length 330;
                                                                                                                              4; Indels
                                                                                                        DB 5;
                                                                                                                   Pred. No. 2e-122;
3; Mismatches
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                                                                                                       Score 1729;
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                                                                                                      98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                   Best Local Similarity 97.9
Matches 323; Conservative
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                                                                                  Sequence 330 AA;
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                                                            the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                        Query Match
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The invention relates to a method for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. The mediated condition or a Th2 cell mediated condition in a mammal. The composition comprising a death domain containing receptor (DR6) agonist cor antagonist. The method is useful for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. A DR6 agonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with aberrant apoptosis, graft or preventing at least one symptom associated with aberrant apoptosis, graft versus-host disease, vasculitis, poorlasis, parcreating, insulindependent diabetes mellitus, cancer, multiple sclerosis, Hashimoto's chyroiditis, Graves disease, transplant rejection, systemic lupus crythematosus, autoimmune dermatosus, autoimmune cardiopathy, autoimmune crimatosis, autoimmune dermatosis, autoimmune cardiopathy, autoimmune crimatosis, autoimmune crimatosis, hashimoto's disease, organ rejection after transplantation, thrombotic curaemic syndrome (HUS), aplastic anaemia myelodysplasia, multiple organ dysfunction syndrome (MUS), adult respiratory distress syndrome (ADS), adult respiratory distress syndrome (ADS), contaction syndrome (MUS), adult respiratory distress syndrome (ADS), contaction syndrome (ADS), adult respiratory distress syndrome (ADS), infaction, compilcations of infactions of infaction syndrome (ADS), tulninant viral hepatitis furnome and incompant of syndrome (ADS), contaction of syndrome (ADS), distributed lymphoma, HUV-induced lymphoma, HUV-induced lymphoma, HUV-induced lymphoma, HUV-induced lymphoma, HUV-induced lymphoma, HUV-indu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated ulceration, cytoprotection during cancer treatment, teroperation from chemotherapy, recuperation from irradiation therapy, or a condition or symptom related to the above mentioned diseases in a mammal. The present sequence is human DR6 protein-related protein
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Treating or preventing T cell or Th2 cell mediated condition e.g., asthma or multiple sclerosis in mammal, comprises administering composition comprising death domain containing receptor, DR6 agonist or antagonist.
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ANO. 2e-122;
4; Indels
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3; Mismatches
                                                                                                                                                     Disclosure; Page 132-133; 133pp; English.
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Local Similarity 97.9%;
hes 323; Conservative
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GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG

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ABB81641;

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Human IgG gamma 1 heavy chain SEQ ID NO:15.
                                                                                                  28-NOV-2000; 2000US-0253561P. 07-FEB-2001; 2001US-0267211P.
                                                                                           28-NOV-2001; 2001WO-US044808
          (first entry)
                                                                                                             (ZYMO ) ZYMOGENETICS INC
                                                                                                                    Presnell SR, Xu W,
                                                                                                                           2002-527700/56.
                                                                                                                                N-PSDB; ABQ73076
                                                                                                                                                                                                                                           Sequence 330 AA;
                                                                            WO200244209-A2
                                                                     Homo sapiens.
          25-SEP-2002
                                                                                   06-JUN-2002
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The present invention describes an isolated human zcytor19 protein (I),
and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
antitheumatic, antiatrhitic, neuroprotective, antiinflammatory,
antidiabetic, nephrotropic, dermatoJogical, anti-HIV and haemostatic
activities, and can be used in vaccines. (I) or an antibody binding (I)
cactivities, and can be used in vaccines. (I) or an antibody binding (I)
cc activities, and can be used in vaccines. (I) or an antibody binding (I)
cc activities, and can be used autoimmune system for reducing rejection of
tissue or organ transplants and grafts and for treating T-cell specific
cleakaemias or lymphomas and autoimmune system for reducing rejection of
cleases and Crohn's disease. The antibodies can also be used for treating
disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or
cyasculitis associated with lupus, polyarteritis, scleroderma, HIV-related
clisease, amyloidosis and haemolytic uraemic syndrome. (I) and the
antibodies can also be used for renal or urological neoplasms and
cliseases, Human zcytor19 is located to chromosome 1, more specifically to
chromosome 1p36.11. The present sequence represents a human Igg gamma 1
contains the present
contains the present
contains the present
Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic; vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus; autoimmune disease; rheumatory bowel disease; corhu's disease; asthma; immunologic renal disease; antidis; moultiple sclerosis; HIV; mesangioproliferative disease; chronic lymphocytic leukaemia; bornchitis; mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis; haemolytic uraemic syndrome; renal neoplasm; urological neoplasm; emphysema; chronic airway disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel Zyctor19 polypeptides and polynucleotides useful for stimulating immune responses in animals for producing antibodies, and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grant FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whitmore TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases, leukemia and asthma.
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180
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                                                                  PSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
                                                                                                                                                                                                Zcytor17; chromosome 5; Sql1; cytokine receptor; immunomodulatory; antiinflammatory; antiiviral; antirheumatic; antiarthritic; cytostatic; antiinflammatory; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatorid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antinflammatory, antiviral, cytostatic, antirtrentic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating or such as in the treatment of infections involving immunosuppression, including certain viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynucleotide encoding a cytokine receptor zyctor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders.
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                              LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
                                             PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                               STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.
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                                                                                                                                                                                                                                                                  301 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
                                                                                                                                                                                                                                                QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                                                                                                                                                                                                                                                                    ABB05736 standard; protein; 330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2000; 2000US-0214282P.
29-JUN-2000; 2000US-0214955P.
08-FEB-2001; 2001US-0267963P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-090519/12.
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ABB05736
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Gaps ö

5; Length 330; 4; Indels

Score 1729; DB 5; Pred. No. 2e-122; 3; Mismatches 4

Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPBPVTVSWNSGALTSGVHTFPAVLQSS 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS

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15-JUN-2001; 2001US-0298710P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, fusion protein, 1gE Fcepsilon, 1gG Fcgamma, FcepsilonRI, allergy, FcepsilonRII, FcgammaRIIB; protein therapy, 1gE, 1gG, asthma, hay fever, allergic asthma, allergic rhinitis, hay fever; food allergy; atopic dermatitis, drug allergy, peanut allergen.
           for
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                                                                                                                                                                                                                                               PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYVDGVEVHNAKTKPREEQYN
infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful freating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the Sqll chromosomal region. ABA93767 tc ABA893843 and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention
                                                                                                                                                              1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                       GLYSLSSVVTVPSSSLGQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                   PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                                                                                                                                                           STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                       STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDE
                                                                                                                                                   1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                            GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                              5; Length 330;
                                                                                                                                 Indels
                                                                                                           Score 1729; DB 5;
Pred. No. 2e-122;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                     QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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/label= Hinge_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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|abel= CH1 region
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/label=_CH2_region
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/label= CH3_region
                                                                                                                                 3;
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                                                                                                             98.0%;
llarity 97.9%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 1gG1 Fcgamma region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                       Similarity
                                                                                           Sequence 330 AA;
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The invention relates to a novel fusion protein comprising an IgE Feepsilon fragment and an IgG Fegamma fragment, which binds to an FeepsilonKI and/or FeepsilonKII receptor and an FegammaRIB receptor. The fusion protein of the invention may have a use in protein therapy. The fusion protein is useful in treating or preventing IgE-mediated allergies and asthma, such as allergic asthma, allergic rhinitis, hay fever, food allergy, atopic dermatitis and drug allergy. The allergic response is particularly caused by peanut allergen. The present sequence represents the human IgGI Fegamma fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                            New fusion protein which binds to FcepsilonRI or RII receptor and FcgammaRIE receptor, useful for treating or proventing allocation
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Pred. No. 2e-122;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                               Disclosure; Fig 5; 32pp; English.
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AAE32915 standard; protein; 330
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97.9%;
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                                                                                                            WPI; 2003-167440/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
(TANO-) TANOX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 330 AA;
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                                                       Wu H,
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Reducing the immunogenicity of a fusion protein by changing an amino acid within the junction region spanning a fusion junction of a fusion protein to reduce the ability of the candidate T-cell epitope to interact with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method of reducing the immunogenicity of a fusion protein. The method involves identifying a candidate T-cell epitope within a junction region spanning a fusion junction of a fusion protein and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of fusion proteins for use in therapy. The present sequence is human immunoglobulin G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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3; Mismatches
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Matches 323; Conservative
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                                           WO200279415-A2
    Homo sapiens.
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                                                                                                                                                                                                                    Reducing the immunogenicity of a fusion protein comprises changing a manno acid within the junction region to reduce the ability of the candidate T-cell epitope identified within the junction spanning to interact with T-cell receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Match 98.0%; Score 1729; DB 6; Length 330; Local Similarity 97.9%; Pred. No. 2e-122; les 323; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunoglobulin G1 (IgG1) heavy chain Fc region
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30-MAR-2002; 2002WO-US009815
                                                                                     (LEXI-) LEXIGEN PHARM CORP.
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given in the exemplification of the present invention

Human, DR6, B-cell mediated disease; immunosuppressive; antirheumatic; antiarthritic; antiasthmatic; dermatological; antiinflammatory; antipacoriatic; antidiabetic; cytostatic; neuroprotective; thyromimetic; antithyroid; neuroprotective; thyromimetic; antithyroid; nephrotropic; antiinfertillty; vasotropic; virucide; hepatotropic; antibacterial; antiulcer; haemostatic; antianaemic; antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity.

Homo sapiens.

WO2003051290-A2.

26-JUN-2003

10-DEC-2002; 2002WO-US037596

17-DEC-2001; 2001US-0342632P

& CO ELI (ELIL) LILLY ä Yang Song HY, Na S, Liu J,

WPI; 2003-541604/51.

Treating or preventing a B cell mediated condition e.g., chronic hepatitis or chronic cirrhogis, in a mammal by administering a pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to the mammal.

Disclosure; Page 96-97; 97pp; English.

The present invention describes a method (MI) for treating or preventing composition composition a mammal by administering a pharmaceutical composition composition and a mammal by administering a pharmaceutical composition comprising at least one by a flood described: (I) inhibiting B cell mediated immunity in a mammal. By administering a pharmaceutical composition comprising at least one DRG agonie: (2) use of a DRG agonist in the manufacture of a medicament for treating or preventing at least one space of a medicament for treating or preventing at least one space of a produced architist, serhma, eczema, inflammacory bowel disease, cancer, vasculitie, psoriasis, multiple solerosis, Habinoco's thyroidiis, Graves disease, transplant rejection, systemic lupus erythemacosus, Behcet's disease, transplant rejection, foronic populamune infectility, autoimmune gestriis, autoimmune peptropathy, autoimmune hepatitis, chronic negration after transplants of mornic conditions, autoimmune peptropathy, autoimmune hepatitis, chronic foronic organic conditions, autoimmune dermatosis, fibrosing lung disease, fulminar viral hepatitis, chronic foronic organic cransplants of mornic conditions, and at least one condition or syndrome (MBS), adulated myslodysplasia, multiple organ dysfunction syndrome (MBS), adulated myslodysplasia, multiple organ dysfunction syndrome (MBS), adulated to the conditions in a mammal,; and (3) use of DRG antagonist in the manufacture of a medicament for treating or preventing at least one symptom associated with conditions (C2) such as aberrant apoposis, immunosuptomes, in a mammal,; and infection, complications of infection, willy HIV, HIV, Induced ADS, fulminant viral hepatitis and infection complications of infection, and infection for proprotection during can be part in the manufacture of a med

ô The invention provides human antibodies that bind to stem cell factor (SCF) protein. SCF is also known as mast cell growth factor, steel factor or c-kit ligand. Antibodies of the invention are useful for preparing compositions for treating asthma. They are also used in gene therapy. The present sequence is human SCF antibody heavy chain constant region 180 180 240 241 ITKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300 9 Human, antibody, stem cell factor; mast cell growth factor; asthma; SCF; steel factor; c-kit ligand; gene therapy; heavy chain. GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW STYRVVSVLTVLHQNWANGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE Gapa stem cell factor protein, ö Length 330; 4; Indels to stem cell fac treating asthma. Human A2-G8 SCF antibody heavy chain constant region. 9 Score 1729; DB 6; Pred. No. 2e-122; QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330 3; Mismatches New purified human antibody that binds useful for preparing a composition for Example 10; Page 47-48; 94pp; English. Tomkinson A, Neben S; Ą AAO31102 standard; protein; 330 16-DEC-2002; 2002WO-US040227. 17-DEC-2001; 2001US-0342174P. 98.0%; 97.9%; (first entry) Conservative WPI; 2003-523500/49. Query Match Best Local Similarity (FARB) BAYER CORP N-PSDB; AAL62618 Sequence 330 AA; WO2003051311-A2. Homo sapiens Takeuchi T, 06-OCT-2003 26-JUN-2003 Matches 323; 61 61 121 121 181 AA031102; 181 241 301 RESULT 12 AA031102 ខ្លង្គខ្ល 셤 엄 엄 ò 셤 8 ઠે 8 ò ઠે 셤

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antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular meovascular disease, obesity, haemangioblastoma, haemangioblastoma, arteriosclerosis, inflammatory disorders, atherosclerosis, endometriosis, neoplastic inflammatory disorders, atherosclerosis, endometriosis, neoplastic sequence represents a human IgGl constant region of an anti-Ang-2 antibody
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                                                                                                                                                                                                                     6; Length 330;
                                                                                                                                                                                                                 Score 1729; DB 6; Length 3
Pred. No. 2e-122;
3; Mismatches 4; Indels
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12-APR-2002; 2002US-0371966P.
                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the
                                                                                                                                                                                                   GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                     PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                         STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                        LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
                                                                                                                             1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                               STYRVVSVLTVLHQN#MNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer; angiogenesis; antibody; human.
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                                                           ); DB 6; Length 330;
2e-122;
thes 4; Indels
                                                           Score 1729; DB
Pred. No. 2e-12
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-Ang-2 antibody IgG1 constant region
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                                                           Match 98.0%;
Local Similarity 97.9%;
les 323; Conservative
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                            Sequence 330 AA;
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                                                            Query Match
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N-PSDB; ADF11388
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Job time : 220.58
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                                         The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index of such fusion protein comprises a non-interleukin-2 (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a composition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is human immunoglobulin gamma (IgG) constant region. This sequence is used to illustrate the method of the invention
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                                                                                                                                                                                                                                                          GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder; osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder; osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huang
                                                                                                                                                                                          ;
                                                                                                                                                                    6; Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martin F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.
                                                                                                                                                                                         4; Indels
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                                                                                                                                                                   Score 1729; DB 6;
Pred. No. 2e-122;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         OCGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                      51-53; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sullivan JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADF11389 standard; protein; 330 AA
  or immune disorders
                                                                                                                                                                   98.0%;
97.9%;
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                                                                                                                                                                  Query Match
Best Local Similarity 97.9
Matches 323; Conservative
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                       Page
                                                                                                                                               Sequence 330 AA;
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                       Example 1;
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The present invention describes an isolated human antibody (I) that specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of (I); (2) methods of treating an osteopenic disorder in a patient, comprising administering to a patient the pharmaceutical composition of (I) or a pharmaceutical amount of (I); and (3) a method composition of (I) or a pharmaceutical amount of (I); and (3) a method composition of (I) or a pharmaceutical amount of (I); and (3) a method can detecting OPGL, and measuring the level of bound antibody in the sample. (I) has osteopathic, antiarthritic and cytostatic activities, and can be used in treating bone disorders, such as osteoporosis, bone loss from arthritis, pager's disease or osteopenia. The antibody (I) may also be used for detecting OPGL in biological samples and in identifying cells or tissues that produce the protein. The present sequence represent a sequence which is used in the exemplification of the present invention.
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New isolated antibody that specifically binds osteoprotegerin ligand, useful for diagnosing or treating bone disorders, such as osteoporosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1729, DB 7; Length 330;
Pred. No. 2e-122;
3; Mismatches 4; Indels
                                useful for diagnosing or treating bone disorders, such a
bone loss from arthritis, Paget's disease or osteopenia.
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                                                                                                                 Example 3; SEQ ID NO 2; 156pp; English.
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

February 22, 2006, 21:31:15 ; Search time 33.6269 Seconds (without alignments) 944.229 Million cell updates/sec Run on:

US-10-000-439-2

1764 1 ASTKGPSVFPLAPSSKSTSG........MHEALHNHYQQRSLSLSPGK 330 score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Description	Ig gamma-1 chain C	Ig gamma-3 chain C		chain	Ig gamma-4 chain C	Ig heavy chain V r	Ig gamma 2a chain	Ig gamma-1 chain C	Ig gamma 2b chain		Ig gamma 1 chain c	Ig gamma chain Cr		Ig gamma-2 chain C	Ig gamma-1 chain -	Ig heavy chain pre	hain	-	Д	monoclonal antibod	gamma-1	g gamma-1	g gamma-3	g gamma-1	מ	σ	g gamma-2a	д датта-2а	-
SUMMARIES		DH.	A23511	A60764	B	F	869339	147159	S31866	147160	PT0207	147158	RB	147161	an	S31459	2080	C30554	G3HUWI	PS0018	PC4436	PS0017	AIS.	G3MSC	GIMSM	G3MSM	G2MSA	S37483	G2MSAB	G2MSAM
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	Length	330	377	377	326	327	374	328	255	328	234	328	323	328	329	472	470	308	289	333	444	326	324	329	393	398	330	469	335	399
d	Query Match	98.0	90.3	90.5	88.8	88.0	69.5	69.4	69.3	69.1	68.9	9. /9	67.6	67.4	9.99	0.99	64.9	63.8	63.7	63.4	63.3	63.2	62.9	62.8	62.6	62.2	62.0	-	61.8	61.7
	Score	1729	1592.5	1590.5	1566	1552.5	1225.5	1225	1222	1219	1216	1193	1192.5	1189			1144.5	1125.5	1123	1117.5	1116	1114	1109	1108	1104	1097	1093	1093	。	1088
	Result No.	1	7	Ю	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

Ig gamma-2c chain Ig gamma-2a chain	19 gamma-za chain 19 gamma-2 chain C 19 gamma-2b chain	Ig gamma-2b chain Ig gamma-2b chain	ig gamma 4 chain c Ig gamma heavy cha Ig epsilon chain C	Ig heavy chain VHI Ig heavy chain V-I	
S00847 S40295	FS0019 S06611 G2MSBM	S01321 G2MS11	147162 146732 S38864	S69340 A36040	S14236 A4944 S69131
0 00	7 77 71	24	N 10 10	0 0 0	9000
329 446	322 327 405	475	277 180 548	249 218	152 220 241
61.5	50.3	8.83 6.83	37.9 36.8	31.0	30.7
1085.5	1063.5 1054	1039	1028 669 648.5	549 547	5342 3342 3242
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ALIGNMENTS

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RESULT 1
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Gramma-1 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: J3-J3n-1981 #sequence revision 18-Aug-1982 #text_change 09-Jul-2004 C;Accession: A94433; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R;Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982 A;Ftlle: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Ftlle: The nucleotide sequence of a human immunoglobulin C-gammal gene.

A;Accession: A93433
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Motes: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:217370
A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,
A;Note: Lys-330 is removed after translation
B;Haris L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904

A;Accession: A90564
A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 136-154, (2', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240
A;Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240
A;Cross-references: UNIPARC: UPI000017378B
A;Note: this sequence has the Gim(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.

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A,Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPARC:UP1000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27.
C;Genetics:
A;Gene: GDB:IGHG3
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                                                                                                                                                                                                    Gramma-3 chain C region (allotype G3m(b)) - human
GrSpecies: Homo sapiens (man)
GrSpecies: Allots and the sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
GrAccession: A21511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1989
Aritle: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507; PMID:3081877
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C;Species: Homo sapiens (man)
C;Species: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an 3,Reference number: A60764; MUID:90007613; PMID:2571587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
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A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/5; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 ALHNHYQQRSLSLSPGK 330
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A;Status: preliminary
A;Molecule type: DNA
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A; Introns: 99/1; 114/1; 224/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap thain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology < IM2>
F; 21-35/Domain: immunoglobulin homology < IM2>
F; 23-310/Domain: immunoglobulin homology < IM3>
F; 27-83; 144-204, 250-308/Disulfide bonds: #status experimental
F; 109/loisulfide bonds: interchain (to light chain) #status experimental
F; 109/112/Disulfide bonds: interchain (to heavy chain) #status experimental
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A;Residues: 1-96, "R', 98-197, "D', 199-218, "E', 240, "M', 242-266, "D', 268-271, "D', 273-330 <SCH
A;Residues: 1-96, "R', 98-197, "D', 199-218, "E', 240, "M', 242-266, "D', 268-271, "D', 273-330 <SCH
A;Cross=references: UNIPARC: UPI0000173790
A;Cross=reference has the Glm(3) and Glm(non-1) markers
B;Gall, W.E.; Edelman, G.M.
B;Gall, W.E.; Edelman, G.M.
A; 3188-3196, 197, G. a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Contents: annotation; disulfide bonds
A;Contents: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A;Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                             , 27
                                                                                                                                                                                                                                                                                                                                                                                                                                           KO
                                  Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)
Jen Primaerstruktur
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                                                                                                             Reference number: A91668; MUID:77070269; PMID:826475; Contents: myeloma protein Nie
           Chem. 357, 1571-1604, 1976
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A;Cross-references: GDB:120085; OMIM:147100
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           Hoppe-Seyler's Z. Physiol.
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A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
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C; Complex: An immunoglobulin hererotetramer subunit consists of two identical light (kai hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l. C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology < LML>
F; 20-85/Domain: immunoglobulin homology < LML>
F; 213-202/Domain: immunoglobulin homology < LML>
F; 213-202/Domain: immunoglobulin homology < LML>
F; 214/Disulfide bonds: interchain (to light chain) #status experimental
F; 27-83; 140-200, 246-304/Disulfide bonds: #status experimental
F; 210-21, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 27-83; 140-200, 246-304/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 27-85; 20-85/Domain: managemental
F; 20-85/Domain: manage
                             R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Ittle: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A;Reference number: A93132; MUD:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
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Biochem. J. 121, 217-225, 1971
A,Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A,Reference number: A90253; WID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A,Title: Structural studies of immunoglobulin G.
A,Title: Structural studies of immunoglobulin G.
A,Reference number: A93157; MUID:69064124; PMID:5782707
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89.1%; Pred. No. 2.8e-102;
cive 15; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
                                                                                                                                                                                                                                         A,Molecule type: protein
A,Reaidues: 238-275 <HOF>
A,Cross-references: UNIPARC:UP10000173794
                                                                                                                                                                                                                                                                                                                                                 R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
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                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                        Length 377;
                                                                                                                                                                                                                                                                               Indels
                             ;Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B;Superfamily: immunoglobulin homology;Keywords: immunoglobulin;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                    Query Match 90.2%; Score 1590.5; DB 2. Best Local Similarity 80.1%; Pred. No. 6.6e-104; Matches 302; Conservative 13; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV-
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361 ALHNRFTQKSLSLSPGK 377
Residues: 1-377 <HUC>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Residues: UNIPARC:UPI0000115524; EMBL:U03779; NID:9433123; PIDN:AAA52217.1;
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: Sus scrofa domestica (domestic pig)
C;Date: Sus scrofa domestica (domestic pig)
C;Date: Sus scrofa domestica (domestic pig)
C;Accession: 147159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158; MUID:95015845; PMID:7930579
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Tile: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVF 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 TQTYICNVN-----HK-PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.5%; Score 1225.5; DB 2; Length Best Local Similarity 87.1%; Pred. No. 2.2e-78; Matches 230; Conservative 6; Mismatches 17; Indels
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.larity 67.5%; Pred. No. 2e-78;
Conservative 46; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Katus: preliminary
A; Molecule type: mRNA
A; Readues: 1-140, CC', 142-374 <KH2>
A; Cross-references: UNIPARC: UPI0000176F25; EMBL: X81695
C; Superfamily: immunoglobulin C region; immunoglobulin
                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695 R;Khamlichi, A.A. submitted to the EMBL Data Library, September 1994 A;Reference number: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S72664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 PSVFLFPPKKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNMYVDGVEVHNAKTKPREEQFN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STYRVVSVLTVIHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSVFLFPPKPKDTLMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
                    g gamma-4 chain C region - human
Species: Homo eapises (man)
Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
Accession: A90933; A90249; A02150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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88.8%; Pred. No. 2.5e-101;
ive 15; Mismatches 19; Indels 3;
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A;Molecule type: protein
A;Realdues: 1-30;81-326 <PIN>
A;Cossereferences: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C;Genetics:
                                                                                                                                                                                                       A;Title: Nuclectide sequence of a human immunoglobulin C-gamma4 ;
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Accession: A90933
A;Accession: A90933
A;Accession: A90933
A;Accession: A90933
A;Accession: A90933
A;Accession: A90934
A;Cession: A90934
A;Cession: A90947190
A;Accession: A90947190
A;Accession: A90949; MUID:70207560; PMID:4192699
A;Reference number: A90249; MUID:70207560; PMID:4192699
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                                                                                                                                              Ellison, J.; Buxbaum, J.; Hood, L.
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A;Molecule type: mRNA
A;Residues: 1-328 «KAC»
A;Cross-references: UNIPARC:UP10000115525; EMBL:U03780; NID:g433125; PIDN:AAA52218.1; P
C;Genetics:
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C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Accession: PTO207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PTO207; MUID:91287716; PMID:2062315
A;Accession: PTO207
A;Molecule type: mRNA
A;Residues: 1-234 < ERR>
A;Cross-references: UNIPARC:UPI0000176F05
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGSFFLYSKLTVDKS 298
                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                   1 APKTAPLVYPLAPCGRDTSGPNVALGCLASSYFPBPVTVTWNSGALTSGVHTFPSVLQPS
                                                                                                                                                                                                                                                                                                                                                                       GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                  1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                              Length 328;
                                                                                                         A;Gene: 1gG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                           58;
                                                                                                                                                                                            ; Score 1219; DB 2;
; Pred. No. 5.2e-78;
45; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1216; DB 2;
Pred. No. 5.5e-78;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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ilarity 67.2%;
Conservative 4
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Best Local Similarity 95.7%;
Matches 224; Conservative
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Best Local Similarity
Matches 223; Conserv
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C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C.Accession: 147160
C.Accession: 147160
J. Immunol. 153, 3565-3573, 1994
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences (A.Reference number: 147158; MUID:95015845; PMID:7930579
A.Accession: 147160
A.Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.More: Homo spaniers.
A.More: Homo spaniers of man) gene engineered and expressed in Escherichia coli
C.Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C.Accession: S31866
B.Filpula, D. submitted to the EMBL Data Library, February 1993
A.Description: Screeing method for protein-protein interactions of cloned gene 1 A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Coross-references: UNIPARC:UP1000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA498:
C.Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:33-255/Region: human 1g gamma-1 chain C region
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                                                                                                                                                                                                                                                                                                          TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 151
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                        GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                               PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                  PSVFIFPPREXEMPLALSRIPQVICTVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN
                                                                                                                                                                                                                   STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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A; Residues: 1-47,'E',49-71,'PV',72-128 < PRA>
A; Residues: 1-47,'E',49-71,'PV',72-128 < PRA>
A; Cross-references: UNIPRAC: UP100001737B

R; Martens, C.L.; Moore, K.W.; Steinmerz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A; Mille: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain games of rabbit IgG; isolation of a cDNA encoding gamma heavy chain games of rabbit IgG; isolation of a cDNA encoding gamma heavy chain games of rabbit IgG; isolation of a cDNA encoding gamma heavy chain games of rabbit IgG; isolation of a cDNA encoding gamma heavy chain with the same of rabbit IgG; isolation of a cDNA encoding gamma heavy chain with the same control of the section of section of the els allotypic marker, 104-Met, and the els allotypic marker, R; Fruchter, R.G.; Jacken, S.A.; Mole, L.B.; Porter, R.R.

R; Fruchter, R.G.; Jacken, S.A.; Mole, L.B.; Porter, R.R.

R; Fruchter, R.G.; Jacken, S.A.; Mole, L.B.; Porter, R.R.

A; Notect this sequence at uniper; Apropriation of the heavy chain of rabbit immunoglobulin A; Residues: 132-14; E. 145-161 c FRUD

A; Residues: 132-13; E. 145-161 c FRUD

A; Residues: 129-13; E. 145-161 c FRUD

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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147161
Bixeskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
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C;Species: Oryctolagus cuniculus (Gomestic rabbit)
C;Species: 24-Apr-1994 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C;Date: 24-Apr-1994 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C;Accession: A91749; A90290; A99288; A90245; A94416; A02<u>1</u>61
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot A;Reference number: A91749; MUID:84030930; PMID:6313520
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A;Residues: 1-323 <BER>
A;Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A;Oute: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R;Pratt, D.M; Mole, L.E.
Biochem. J. 151, 337-349, 1975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:9433121; PIDN:AAA52216.1;
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                                                                                                                                                       Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Pive putative subclasses of swine IgG identified from the cDNA sequences A;Reference number: I47158; MUID:95015845; PMID:7930579
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                    234
                    PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: 147158
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule typs: mRNA
A, Residues: 1-328 <KAC>
A, Cross-references: UNIPARC:UP10000115523; EMBL:U037
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A,Acceввion: A90290
A,Molecule type: protein
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A; Reference number: A94553
A; Rocession: A94553
A; Rocession: A94553
A; Rocession: B. K.; Hussain, O.Z.; Cebra, J.J.
B; Ribitableth, B. K.; Hussain, O.Z.; Cebra, J.J.
B; Cross-reference number: A90352; MUID:71058471; PMID:5538606
A; Ribitableth, B. K.; Hussain, O.Z.; Cebra, J.J.
B; Cross-reference number: A90352; MUID:71058471; PMID:5538606
A; Rocession: A90352
A; Rocession: A90352
A; Rocession: A90352
A; Rocession: A90353
A; Rocession: A90359
A; Rocess
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a 8 A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-328 < KAC>
A;Cross-references: UNIPARC:UPI0000115526; EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PI
C;Genetics:
A;Gene: IGS
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology < IMM>
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61 GLYSLISMYTVPSSQKAT----CNVAHPASSTKVDKTVEPIRTPZPBPCTCPKCPPPENL 116
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531459
531459
531459
531659
531659
5.5 gamma-1 chain - sheep (fragment)
5.5 species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
6.5 Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
6.5 Accession: 331459
A.Feference number: S31459
A.Accession: S31459
A.Accession: S34459
A.Status: preliminary
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F;24-310/Domain: immunoglobulin homology <IM3>
F;28-9/Disulfide bonds: #status experimental
F;14-202/Disulfide bonds: #status experimental
F;147-8/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental
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A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
A;Molecule type: protein
A;Residues: 134-226 <TRA>
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241 LTKNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLDSVGSFFLYSKLTVDKS 298
                                                                                                                                                    202 GLYSLSSVVTVPASTSGAQTFICHVAHPASSTKVDKRVEPGCPDPCKHC-RCPPPELPGG 260
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                                                                                                                           Gaps
                                                                                                                            3;
                                                                                                Query Match 66.0%; Score 1163.5; DB 2; Length 472; Best Local Similarity 65.7%; Pred. No. 6.3e-74; Matches 218; Conservative 40; Mismatches 71; Indels 3;
A;Molecule type: mRNA
A;Residues: 1-472 <PAT2 <PAT3
A;Residues: 1-472 <PAT9
A;Cross-references: UNIDARC:UPI0000176F35; EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>
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Search completed: February 22, 2006, 21:38:16 Job time : 34.6269 secs

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GenCore version 5.1.7
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February 22, 2006, 21:24:24; Search time 219.43 Seconds (without alignments) 1061.041 Million cell updates/sec Run on:

US-10-000-439-2 1764 1 ASTKGPSVPPLAPSSKSTSG......MHEALHNHYQQRSLSLSPGK 330 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ŧ	рошо	homo	Q569f4 homo sapien	homo	homo	Q6pja4 homo sapien	рошо	homo	7 homo	Q5re17 pongo pygma	homo	homo) homo	рошо	homo	Q6n093 homo sapien	Q6p6c4 homo sapien														
ID	* * * * * * * * * * * * * * * * * * * *	IGHG1_HUMAN	Q6GMX6_HUMAN	Q569F4_HUMAN		Q7Z5W1_HUMAN	Q6PJA4_HUMAN		Q6GMW7_HUMAN	Q6GMX1 HUMAN	Q6IN78_HUMAN	Q6N089_HUMAN	Q6P055 HUMAN	Q6MZQ6_HUMAN	Q6N094 HUMAN	Q6N097_HUMAN	Q7Z351_HUMAN	Q6N096_HUMAN	Q6PYX1_HUMAN	Q6PI81_HUMAN	Q6PJF1_HUMAN	Q6N095 HUMAN	Q6PJ95_HUMAN		Q5RE17_PONPY	Q6N030_HUMAN	OSEBM2_HUMAN	Q8N4Y9 HUMAN	Q8NF17 HUMAN	IGHG2 HUMAN	Q6N093 HUMAN	Q6P6C4_HUMAN
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& Query Match	1 1 1 1	98.0	98.0	98.0	ъ.			98.0					97.8			97.8		97.6			97.5	97.4	97.4				90.3			8	•	88.5
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ALIGNMENTS

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MEDIATE-7070269; PubMed-826475;
MEDLINE-77070269; PubMed-826475;
PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).
MEDLINE-77070269; PubMed-826475;
Ponstingl H., Hilschmann N.;
The rule of antibody structure. The primary structure of a monoclonal reprides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).

KI Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).

MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Unug H.-D., Palm W., Hilschmann N.;
Schmidt W.E., Unug H.-D., Palm W., Hilschmann N.;
Schmidt W.E., Unug H.-D., Palm W., Hilschmann N.;
Structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE OF 1-135 (MYELOWA PROTEIN EU).
PROTEIN SEQUENCE OF 1-135 (MYELOWA PROTEIN EU).
PROTEINS=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
Biochemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                      NUCLES SEQUENCE.
NUCLES 2274238; PubMed=6287432;
Ellison J.W., Berson B.J., Hood L.E.;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; Biochemistry 9:3171-3181(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
PROTRIN SEQUENCE OF 136-329 (EU).
MEDLINE-71064025; PubMed=5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                             330 AA
                             PRT;
                                                                                                                       Ig gamma-1 chain C region.
Name=IGHG1;
                             STANDARD;
                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                             HUMAN
                                              P01857;
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1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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/FIId=VAR 003886.
D -> E (in GlM(non-1) marker).
FIId=VAR 003887.
L -> M (in GlM(non-1) marker).
/FIId=VAR_003888.
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N-linked (GlcNAc. . .).
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Pred. No. 6e-119;
3; Mismatches 4;
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Best Local Similarity 97.9%;
Matches 323; Conservative
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                                                                                                                                                                                                                MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal 1g21 immunoglobulin (upstome protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Roppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.
              Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GG GG:0005624; C:membrane fraction; NAS.
GG; GG:0005625; F:antigen binding; TAS.
GG; GG:0008955; P:immune response; NAS.
InterPro: IPR00110; Ig-like.
InterPro: IPR003597; Ig_Cl.
InterPro: IPR003006; Ig_MHC.
Ffam; PF07654; CI-set; 3.
PROSITE; PS0835; IG_LKE; 3.
PROSITE; PS0835; IG_MKC; 2.
3D-structure; Direct_protein sequencing; Glycoprotein; Immunoglobulin C region; Immunoglobulin G media.
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                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE=81208100; PubMed=7236608;
  MEDLINE=71064027; PubMed=4923144;
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A/B=106-330.
A/B=106-329.
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A=121-326.
H/Kx1-330.
B/D=1-103.
A/B=107-330.
A/B=119-330.
A/B=119-330.
A/B=119-330.
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B/H=1-101.
H=1-101.
H=1-101.
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PDB; IAA7; x-ray; H=1-103.

PDB; IDACK, x-ray; H=1-101.

PDB; IDSI; x-ray; H=1-101.

PDB; IECX; x-ray; A/B=106-329.

PDB; IECX; x-ray; A/B=106-329.

PDB; IECX; x-ray; A/B=106-329.

PDB; IFCX; x-ray; A/B=106-329.

PDB; ITX; x-ray; A/B=107-330.

PDB; ITX; x-ray; A/B=107-330.

PDB; IIX; x-ray; A/B=107-330.

PDB; IIX; x-ray; A/B=107-330.

PDB; IDX; x-ray; A/B=107-330.

PDB; IDX; x-ray; A/B=107-330.

PDB; ICX; x-ray; A/B=107-330.
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GHG1 protein.
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Best Local S:
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                             STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGGMX6 HUMAN PRELIMINARY;
QGGMX6;
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TISSUE=Lymph,

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausheer R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L. H., Darge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Fermer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Chards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                        Length 465;
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SMART; SM00409; IG; 2.
SMART; SM00409; IGG1, 3.
SMART; SM00406; IGG1, 3.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypochetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                 98.0%; Score 1729; DB 2; 97.9%; Pred. No. 9.3e-119; ative 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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Q569F4;
                                                                                                                                                                                                                                                                                                                                                Matches 323; Conservative
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                                                                                                                                                                                                                                                                                                                      Similarity
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1.17 (1.17)

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCCNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                    Query Match 98.0%;
Best Local Similarity 97.9%;
Matches 323; Conservative
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                                                 cDNA sequences.";
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Q7ZSW1;
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                                                                                              NUCLEOTIDE SEQUENCE
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NIH MGC Projec
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NUCLEOTIDE SEQUENCE.

TISSUE-Splean;

KEDLINE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KIAUSDER S. R. Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raichards S., Worley K.C., Mackernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Mackernan R.J., Malek J.A., Glabbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glabbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahaseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                 120
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
      'Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                    STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                               200 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                      1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                           Length 469;
                                                                                                                                                                                                       Indels
                                                                                                              Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092518; AAH92518.1; -; mRNA.
SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                      Query Match 98.0%; Score 1729; DB 2; Best Local Similarity 97.9%; Pred. No. 9.4e-119; Matches 323; Conservative 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Q7Z7PS;
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                                                                   NUCLEOTIDE SEQUENCE.
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Name=IGHG1;
                                                                                   TISSUE=Lymph;
NIH MGC Proje
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 469;
                                                                                                         NIH MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
HSSP; P01857; HIZH.
SMR; Q727P5; 20-469.
InterPro; IPR003106; Ig-1ike.
InterPro; IPR003306; Ig-1ike.
InterPro; IPR003597; Ig-1.
R PEAM; P07654; C1-8et; 3.
R SWART; SW00406; IGV:
R PROSITE; PS50835; IG_LIKE; 4.
R PROSITE; PS508290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin domain.
SEOUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1729; DB 2;
Pred. No. 9.4e-119;
3; Mismatches 4;
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TISSUB-Primary B-Cells,

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feligodd E.A., Grouse L.H., Derge J.G.,

Ratusherg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A phykins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Perers G.J., Abramon R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubzartne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahking M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raka S.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVPPKSCDKTHTCPPCPAPELLGG
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TISSUB-Primary B-Cells;
NIH MGC Project;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO18747; AAH18747.1; -; mRNA.
HSSP; PO1861; 1ADQ.
SMR; QEDJA4; 20-470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART; SM00409; IG; 2.
SWART; SM00407; IGc1; 3.
SWART; SM00407; IGc1; 3.
SWART; SM00406; IGV; 1.
PROSITE; PS00290; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1729; DB 2;
Pred. No. 9.4e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 9.46
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.76
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Matches 323; Conservative
                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B rownstein M.J., Usdin T.B., Toobliyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley B.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman M., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Rodriguez A. C., Grimwood J., Schmutz J., Myers R.W.,

Rodriguez A., Schen B.D., Myers R.W.,

Rodriguez A., Schmutz J., Myers R.W.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSVFLPPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNVKTKPREBQYN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFLYSKLTVDKSRW 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSVGSFFLYSKLIVDKSRW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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98.0%; Score 1729; DB 2; Length 470;
Best Local Similarity 97.9%; Pred. No. 9.4e-119;
Matches 323; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055984; AAH53984.1; -; mRNA.
HSSP; P01857; 1HZH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam; P07654; C1-set; 3.
SWART; SM00406; IGV; 1.
PROSITE; PS50035; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 2.
Hypotherical protein; Immunoglobulin domain.
SEQUENCE 470 AA; 51204 MW; 778CP34521483E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Spleen;
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Name=IGHG1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYRVVSVLTVLHONWMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE 240
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 PSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaucher C., Klein P., Beliard R.; "Sequence determination of the recombinant human anti-RhD monoclonal antibody T125.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential.
anti-RhD monoclonal T125 gammal heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ### Submitted (JAN-2055) to the EMBL/GenBank/DDBJ databases.

### Submitted (JAN-2055) to the EMBL/GenBank/DDBJ databases.

### InterPro; IPR001599; Ig.

### InterPro; IPR001596; Ig.

### Pfam; PF07654; Cl-set; J.

### RPfam; PF07664; Cl-set; J.

### RPfam; PF07669; IG; 2.

### RPfam; PF07669; IG; 2.

### RPMART; SM00409; IG; 1.

### RPMOSITE; PS00835; IG_LIKE; 4.

#### PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Anti-RhD monoclonal T125 gammal heavy chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1367D400DC7D2859 CRC64;
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                   QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                                             QSEPES HUMAN PRELIMINARY;
QSEPES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jozdan H., Moore T., Max S.L., Wang J., Hasteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Strausberg R.;
Strausberg R.;
Submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.
REMBL; BC073782; AAH73782.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
RICEPTRO; IPR003599; Ig.
RICEPTRO; IPR003110; Ig.
RICEPTRO; IPR003110; Ig.
RICEPTRO; IPR003597; Ig.
RICEPTRO; IPR003597; Ig.
RICEPTRO; IPR003597; Ig.
REPTRO; IPR003597; Ig.
REPTRO; IPR003597; Ig.
REPTRO; SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
REPTRO; IRV0130405; IGV; 1.
REPTRO; IRV0130405; IG.
REPTRO; IGV; 1.
REPTRO; IRV0130405; IG.
REPTRO; IGV; 1.
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                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Best Local Similarity 97.9%; Pred. No. 9.5e-119;
Matches 323; Conservative 3; Mismatches 4:
       475 AA
          PRT;
                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
QGGMW7 HUMAN PRELIMINARY;
QGGMW7;
                                                                                                                                                        Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
           STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                      LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
                                                  386 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073773; AAH73773.1; -; mRNA.
GO; GO: G016021; C.integral to membrane; IEA.
InterPro; IPR001599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig.
InterPro; IPR003506; Ig.
InterPro; IPR003506; Ig.
InterPro; IPR003506; Ig.
InterPro; IPR003506; Ig.
SMART; SM00409; IG. 2.
SMART; SM00409; IG. 1.
SMART; SM00409; IG. 1.
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                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                             QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                    PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
HYPOCHELICAL Procein_
SEQUENCE 476 AA; 52286 MW; 622AA
                                                                                                                                              QGGMX1 HUMAN PRELIMINARY;
QGGMX1;
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TISSUE=Spleen;
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181
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DB 2; Length 476;

98.0%; Score 1729;

Query Match

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

R. Klausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,

R. Klausher R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

R. Altschul S. F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S. F., Jordan H., Moore T., Max S.L., Wang J., Heiseh F.,

B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Stapleton M., Sares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Hilalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A.,

R. Hilalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

R. Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                       446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Journalia, Human).
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires; Primates; Catarrhini, Hominidae,
                                                                                      147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS#NSGALTSGVHTFPAVLQSS
                                                                                                                                                                    207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                      267 PSVFLFPPKDTLMISRTPBVTCVVVDVSHEDPBVKFNWYVDGVBVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                    327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                              STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                              ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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TISSUE=Peripheral Nervous System;
NIH MCC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072419; AAH72419.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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3; Mismatches
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                     3;
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97.98;
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QEIN78;
  Best Local Similarity 97.99
Matches 323; Conservative
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NUCLEOTIDE SEQUENCE.
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Name=IGHG1;
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TISSUE-Peripheral Nervous System;

XT TISSUE-Peripheral Nervous System;

XT TISSUE-Peripheral Nervous System;

XT Staubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XT Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XT Klausher R.D., Colling F.S., Magner L. Shenmen C.M., Schuler G.D.,

XT Klausher R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

XT Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XT Altschul S.F., Jedach H., Moore T., Wax S.I., Wang J., Hsieh F.,

XT Diatchenko L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,

XT Diatchenko L., Marushia K., Farmer A.A., Rubin G.M., Long L.,

XT A Diatchenko L., McEwan R.B., Toshiyuki S., Carninci P., Prange C.,

XT Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XT Richards S., Wolfey D.M., Sodergen R.J., Lu X., Gibbs R.A.,

XT Richards S., Wolfey D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XT Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XT Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XT Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XT Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XT Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XT Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XT Nilalon D.K., Muzny D.M., Schwutz J., Myers R.M.,

XT Nilalon D.K., Warzywinski M.I., Skalaka U., Smailus D.E.,

XT Nilalon J.K., Marzy M.M., Madan A., Schein J.E., Jones S.J.M., Marra M.A.;

XT Nilalon J.K., Marzywinski M.I., Skalaka U., Smailus D.E.,

XT Nilalon J.K., Marzy D.M., Marza M.A.;

XT Nilalon J.K., Marzy D.M., Marzywinski M.I., Shalaka U., Smailus D.E.,

XT Nilalon J.K., Marzy D.M., Marzywinski M.I., Marra M.A.;

XT Nilalon J.K., Marzy D.M., Marzywinski M.I., Smailus D.E.,

XT Nilalon J.M., Madan J.S., Molley R.M.,

XT Nilalon J.M., Madan J.S., Molley R.M.,

XT Nilalon J.M., Madan J.M., Madan J.S., Molley R.M.,

XT Nilalon J.M., Madan J., Marra M.A.;

XT Nilalon J.M., Madan J.M., Madan J.M., Madan J.M., Madan J
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                              143 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                            Length 472;
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00209; IG MHC; UNKNOWN_2.
HYPOCHELICAL protein.
SEQUENCE 412 AA; 51724 MW; 26CB340D0046D279 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
[2]
                                                                                                                                                                                  97.8%; Score 1726; DB 2;
97.6%; Pred. No. 1.6e-118;
ive 4; Mismatches 4;
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                                                                                                                                                                                                                         Best Local Similarity 97.6
Matches 322, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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Bukaryota, Metaroa: (bordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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EMBL; BX640627; CAE45781.1; -; mRNA.
HSSP; P01861; IADQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 466;
InterPro; IPR003599; Ig.
InterPro; IPR00710; Ig-like.
InterPro; IPR003106; Ig_cl.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR004006; Ig_WHC.
InterPro; IPR00400; IG; Z.
SWART; SW00407; IG; Z.
SWART; SW00407; IGcl; 3.
SWART; SW00406; IGv; 1.
PROSITE; PS00395; IG_LIKE; 4.
PROSITE; PS00395; IG_MHC; UNKNOWN 2.
SEQUENCE 466 AA; 50854 MW; 53EBOBCEDEB1076E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686P15220.
Name=DKFZp686P15220.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                  97.8%; Score 1726; DB 2;
97.6%; Pred. No. 1.5e-118;
iive 4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Rectum tumor;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGN089 HUMAN PRELIMINARY;
Q6N089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 322; Conservative
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686001196.
Name=DKFZp686001196;
Homo sapiens (Human)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                        146 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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C TISSUE=Esophagus tumor;

C TISSUE=Esophagus tumor;

TISSUE=Esophagus tumor;

The German Chan M. Wiemann S.;

R Fobo G., Han M., Wiemann S.;

Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640622; CAE45776.1; -; mRNA.

R InterPro; IPR003599; Ig.

R InterPro; IPR003109; Ig-like.

R InterPro; IPR003509; Ig-lig-v.

R Pfam; PR07654; Cl-set; 3.
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                 Length 475;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;
                                                                                                                                                                                                                                                                                             97.8%; Score 1725; DB 2;
97.6%; Pred. No. 1.9e-118;
iive 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           446 QQGNVFSCSVMHBGLHNHYTQKSLSLSPGK 475
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             InterPro; IRR001010; Ig-like.
InterPro; IPR003006; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF07654; Cl-set; 3.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
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Matches 322; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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TISSUB=Escophagus tumor;
The German consortium;
The German Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BX640947; CAE45972.1; -; mRNA.
HSSP; PO1861; 1ADQ.
SMR; Q6MZQ6; 20-475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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             TISSUE-Peripheral Nervous System;

A Strausberg R.;
Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; BCG6820; AAH65820.1; -; mRNA.

R HSSP; P01861; 1ADQ.

R InterPro; IPR001559; Ig.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR003597; Ig.C1.

R InterPro; IPR003597; Ig.C1.

R InterPro; IPR003597; Ig.C1.

R Ffam; PF07654; C1-set; 3.

R SWART; SM00409; IG.J.

R SWART; SM00409; IG.J.

R SWART; SM00409; IG.J.

R R SWART; CHOGO IG. IG.J.

R PROSITE; PS00290; IG.MHC; UNKNOWN_2.

H PROSITE; PS00290; IG.MHC; UNKNOWN_2.

H PROCHELICAL DICCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686G11190.
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Q6MZQ6;
NUCLEOTIDE SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                         211 GLYSLSSVVTVPSSSLGTQTYICNVNHKRSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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N [1]

NUCLECTICE SEQUENCE.

TISSUE=Escaphagus tumor;

THE German cDNA Consortium;

Wamburt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Amin and the consortium;

Manutr R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Amin and the consortium;

Manutr R., Meubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Manutr R., Meubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Manutr R., Meubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Manutr R., Meubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Manutr R., Meubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Manutr R., Meubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Manutr R., Meubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Manutr R., Meubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

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Manutr R., Meubner D., Mewes H.W., Weil B., Amid C.,

Manutr R., Meubner D., Mewes H.W., Weil B., Amid C.,

Manutr R., Meubner D., Mewes H.W., Weil B.,

Manutr R., Mewes H., 
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                                                                                                                                                                                                                                          Query Match
97.8%; Score 1725; DB 2; Length 480;
Best Local Similarity 97.6%; Pred. No. 1.9e-118;
Matches 322; Conservative 3; Mismatches 5; Indels C
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00201 IG_MHC; UNKNOWN_2.
Hypochetical protein.
SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;
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481 AA; 52759 MW; 47220D9E64BDF98B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686H20196.
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Q6N097;
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SEQUENCE 48
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                               Gaps
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 Length 481;
                               Indels
Query Match 97.8%; Score 1725; DB 2; Best Local Similarity 97.6%; Pred. No. 1.9e-118; Matches 322; Conservative 3; Mismatches 5;
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Job time : 222.43 secs
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2, Appli 81, Appli 45, Appli 60, Appli 60, Appli 738, Appli 722, Appli 722, Appli 722, Appli 74, Appli

Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

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LIKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSVGSFFLYSKLTVDKSRW 300
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US-09-047-208-2

Sequence 2, Application US/09847208

Publication No. US20030082190A1

GENERAL INFORMATION:

APPLICANT: Saxon, Andrew

APPLICANT: Zhang, Ke

APPLICANT: Zhu, Daocheng

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

TITLE OF INVENTION: UGO-002A

CURRENT APPLICATION NUMBER: US/09/047,208

CURRENT FILING DATE: 2010-05-01

NUMBER OF SEQ ID NOS: 177

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1764; DB 3;
Pred. No. 1.3e-128;
Mismatches 0;
US-10-480-109-5
US-10-867-58-2
US-10-867-596-31
US-10-937-596-31
US-10-863-373-8
US-10-863-373-8
US-10-901-736-60
US-10-901-736-60
US-11-094-555-38
US-11-094-98-22
US-11-090-846-44
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US-11-090-847-44
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tive 0;
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   ORGANISM: Homo sapiens
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   330;
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TYPE: PRT
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Matches 330
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Sequence 2, Appli
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817.308 Million cell updates/sec
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                                                                                                       February 22, 2006, 21:57:24; Search time 168.705 Seconds
                                                                                                                                                                                1764
1 ASTKGPSVFPLAPSSKSTSG.......MHEALHNHYQQRSLSLSPGK 330
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Sequence
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-698-907-22
US-10-928-305-7
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                    US-10-000-439-2
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Match Length
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                                                                           OM protein
                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                        Run on:
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Gaps

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Length 330; Indels 120

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241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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                                                                                                                 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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            Length 330
                                                 4; Indels
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98.0%; Score 1729; DB 3;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4;
          Score 1732; DB 5;
Pred. No. 4e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/0995898A

Publication No. US20030027253A1

GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: No. US20030027253A1ak, Julia E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Grant, Francis J.
FITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE OF INVENTION OF COMPANY
CURRENT FILING DATE: 2001-11-28
FRIOR FILING DATE: 2000-11-28
FRIOR PELING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
98.2%; Pred. No. *c. 2; Mismatches
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          Query Match
Best Local Similarity 98.2<sup>1</sup>
Matches 324; Conservative
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ORGANISM: Homo sapiens
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SEQ ID NO 15
LENGTH: 330
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APPLICANT: Hinton, Paul R
APPLICANT: Hinton, Paul R
APPLICANT: Hinton, Paul R
APPLICANT: Taurushita, Naoya
TITLE OF INVENTION: Alteration of Fc-Fusion Protein Serum Half-Lives By Mutagenesis
FILE REFERENCE: 0582.0039.NPUS07
CURRENT APPLICATION NUMBER: US/0966,673
CURRENT FILING DATE: 2004-10-15
PRIOR PILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: US 60/561,687
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 77
SEQ ID NOS: 77
SEQ ID NOS: 77
LENGTH: 330
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        US-10-00-439-2

Sequence 2, Application US/10000439

Fublication No. US20030064063A1

GENERAL INFORMATION:

TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES

TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES

FILE REPRENCE: UCO67.004A

CURRENT PILLIOR DATE: 2001-024

FRICR APPLICATION NUMBER: US 99/847,208

FRICR APPLICATION NUMBER: US 09/847,208
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SOPTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20050226864Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-000-439-2
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CORGANISM: HOMO SAPIENS
US-10-966-673-29
                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 330
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: LARRICK, JAMES W.
APPLICANT: MYCOFF, KEITH L.
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REPERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: PCT/US01/13932
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR FILING DATE: 2001-04-28
PRIOR PLING DATE: 2000-04-28
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; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONNTHAN D.
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT PILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR RILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
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97.9%; Pred. No. 6.8e-126;
tive 3; Mismatches 4;
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Pred. No. 6.8e-126;
3; Mismatches 4;
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  Publication No. US20020168367A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 97.9
Matches 323; Conservative
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CORGANISM: Homo sapiens
US-10-269-805-68
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Pred. No. 6.8e-126;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/08892949
Fublication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Clindy A.
APPLICANT: Sprecher, Clindy A.
APPLICANT: Bresnell, Scott R.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Waiper, Joseph L.
APPLICANT: Maurer, Mark F.
ITILE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE BEFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
FRIOR FILING DATE: 2000-06-26
FRIOR FILING DATE: 2000-06-26
FRIOR FILING DATE: 2000-06-29
FRIOR PILING DATE: 2001-08-02
FRIOR PILING DATE: 2001-08-02
FRIOR FILING DATE: 2001-08-02
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US-10-047-542-20
; Sequence 20, Application US/10047542
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Best Local Similarity 97.9%;
Matches 323; Conservative 3
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ORGANISM: Homo sapiens
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US-09-892-949-38
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Sequence 81, Application US/10320231A

Publication No. US20030194405A1

GENERAL INFORMATION:

APPLICANT: Neben, Steven

APPLICANT: Takinson, Adrian

TITLE OF INVENTION: Areament Of Asthma

TITLE REFERENCE: 7430*163

TITLE REFERENCE: 7430*163

CURRENT APPLICATION NUMBER: US/10/320,231A

CURRENT FILING DATE: 2002-12-19
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Publication No. US20030166877A1
| GENERAL INFORMATION:
| APPLICANT: Gillies, Stephen
| TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
| TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
| TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
| TITLE OF INVENTION: LEX-017
| CURRENT APPLICATION NUMBER: US/10/112,582
| CURRENT FILING DATE: 2001-03-30
| PRIOR FILING DATE: 2001-03-30
| NUMBER OF SEQ ID NOS: 59
| SOFTWARE: Patentin version 3.0
| LENGTH: 330
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; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1
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98.0%; Score 1729; DB 4;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4;
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TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
FILE REPERENCE: LEX-020
CURRENT APPLICATION NUMBER: US/10/310,719
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,113
PRIOR FILING DATE: 2001-12-04,066
PRIOR PLING DATE: 2001-12-04,066
PRIOR PLING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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; OTHER INFORMATION: IgG1 constant region US-10-310-719-8
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Publication No. US20030166163A1
GENERAL INFORMATION:
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Matches 323; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: misc
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US-10-310-719-8
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Sequence 2, Application US/10408901

Sequence 2, Application US/10408901

Publication No. US20040023313A1

GENERAL INFORMATION:

APPLICANT: Boyle, William

APPLICANT: Bliot, Robin

APPLICANT: Budlock, Eugene

APPLICANT: Martin, Prancis

TITLE OF INVENTION: Inhibitors

TITLE OF INVENTION: Inhibitors

TITLE OF INVENTION: Inhibitors

FILE REFERENCE: MBHB 01-1145-A

CURRENT FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2
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Best Local Similarity 97.9
Matches 323; Conservative
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US-10-408-901-2
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US-10-408-901-2
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98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels
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US-10-383-902A-6
; Sequence 6, Application US/10383902A
; Sequence 6, Application Wo20030224408A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Mulberg, Jurgen
; APPLICANT: Mulberg, Lurgen
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY
; FILE REFERENCE: 10280-042001
; CURRENT FAPLICATION NUMBER: US/10/383,902A
; CURRENT FILING DATE: 2003-03-07
; PRIOR PILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 58
; SOUTWARE: PRESEQ For Windows Version 4.0
; SEQ ID NO 6
; SEQ ID NO 6
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Pred. No. 6.8e-126;
3; Mismatches 4;
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PRIOR APPLICATION NUMBER: US 60/342,174
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81
LENGTH: 330
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Best Local Similarity 97.9%;
Matches 323; Conservative
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                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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; Sequence 2, Application US/10656769
; Publication No. US20040097712A1
; GERREAL INFORMATION:
    APPLICANT: Varnum, Brian
    APPLICANT: Wite, Alison
    APPLICANT: Wite, Alison
    APPLICANT: Wong, Lu Min
    APPLICANT: Qian, Xueming
    TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
    FILE REFERENCE: 01,1554
    CURRENT APPLICATION NUMBER: US/10/656,769
    CURRENT FILING DATE: 2003-09-05
    NUMBER OF SEQ ID NOS: 79
    SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                               1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS
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                                                   98.0%; Score 1729; DB 4; 97.9%; Pred. No. 6.8e-126; iive 3; Mismatches 4;
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Pred. No. 6.8e-126;
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Best Local Similarity 97.9%;
Matches 323; Conservative 3
                                                                          Best Local Similarity 97.9
Matches 323, Conservative
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US-10-656-769-2
ORGANISM: Homo sapiens
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TYPE: PRT
      ) US-10-257-907-5
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US-10-656-769-2
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APPLICANT: Liu, Jingi
APPLICANT: Liu, Jingi
APPLICANT: Na, Songding
APPLICANT: Song, Ho Yeong
APPLICANT: Yang, Derek Di
ITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
FILE REFERENCE: X-13992
CURRENT APPLICATION NUMBER: US/10/257,907
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                        APPLICANT: Presentl, Scott R.
APPLICANT: Xu, Wenteng
APPLICANT: Xu, Wenteng
APPLICANT: Wo. US20040029228Alak, Julia E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Windsvogel, Wayne R.
APPLICANT: Kindsvogel, Wayne R.
APPLICANT: Kindsvogel, Wayne R.
TITLE OF INVENTION: CYTOKINE RECEPTOR
FILE REPERENCE: 02-10
CURRENT APPLICATION NUMBER: US/10/420,034A
CURRENT FILING DATE: 2003-04-18
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PRESENCE OF WINDOWS Version 4.0
SSOFTWARE: 330
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                  Sequence 15, Application US/10420034A Publication No. US20040029228A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10257907
Publication No. US20040043022A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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US-10-420-034A-15
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LENGTH: 330
TYPE: PRT
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US-10-257-907-5
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Search completed: February 22, 2006, 22:03:08 Job time : 170.705 secs

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                                                                                                                     February 22, 2006, 21:58:19; Search time 17.0984 Seconds (without alignments) 287.324 Million cell updates/sec
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Sequence 5, Al
Sequence 6, Al
Sequence 4, Al
Sequence 71,
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USI0_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USI0_NEW_PUB.pep:*
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd
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US-10-493-909-20
US-10-022-289-11
US-11-105-135-1
US-11-105-141-15
US-11-102-621-7
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US-11-102-621-7
US-11-102-621-7
US-11-102-621-7
US-11-102-621-1
US-11-102-621-1
US-11-102-621-1
US-11-104-536-701
US-11-104-536-701
US-11-072-289-7
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Maximum Match 100%
Listing first 45 summaries
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US-10-866-383-6

Sequence 6, Application US/10886383

Sequence 6, Application US/10886383

Publication No. US20060005571A1

GENERAL INFORMATION:

APPLICANT: Hoffmann-La Roche Inc.

TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and use

TITLE OF INVENTION: thereof

FILE REPRENCE: 21695

CURRENT PILIOR DATE: 2004-07-08

PRIOR APPLICATION NUMBER: EP 03015526

PRIOR FILING DATE: 2003-07-10

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.2
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56, Appl
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US-11-102-621-131
US-11-102-621-132
US-11-124-620-7
US-11-139-499-12
US-11-139-499-12
US-11-139-499-12
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US-11-102-621-70
US-11-102-621-67
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US-11-102-621-119
US-11-102-621-120
US-11-102-621-131
US-11-102-621-131
US-11-102-621-131
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US-11-102-621-131
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   ORGANISM: Homo sapiens
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LENGTH: 330
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  TYPE: PRT
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241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

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LIKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW

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TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING :
FILE REPREBRING: 185831/022, 289
CURRENT APPLICATION NUMBER: US/11/022, 289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531, 752
PRIOR APPLICATION NUMBER: US 60/531, 752
NUMBER OF SEQ 10 NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NO 11
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Pred. No. 2.8e-132;
3; Mismatches 4;
                                             Query Match 98.0%; Score 1729; DB 6; Best Local Similarity 97.9%; Pred. No. 2.8e-132; Matches 323; Conservative 3; Mismatches 4;
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; Publication No. US20050249723A1
; GENERAL INFORMATION:
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Best Local Similarity 97.9%;
Matches 323; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-289-11
ORGANISM: Homo sapiens
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US-10-982-440-68
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241 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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; Sequence 68, Application US/10982440
; Publication NO-20060018909A1
; Publication NO-20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Kohn
; APPLICANT: Graham, Kohn
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; TILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-111-04
; PRIOR APPLICATION NUMBER: 60/620,161
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 330;
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Pred. No. 2.8e-132;
3; Mismatches 4;
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Best Local Similarity 97.9%;
Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Homo sapiens
US-10-493-909-20
                                                      -10-493-909-20
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LENGTH: 330
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APPLICANT: Hinton, Paul R.
APPLICANT: Tsurushita, Naoya
APPLICANT: Tsurushita, Naoya
APPLICANT: Tsurushita, Naoya
APPLICANT: Tsurushita, Naoya
APPLICANT: Vasquez, Maximilliano
TITLE OF INVENTION: ALTERATION OF FCRN BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ANTHEODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.000503
CURRENT APPLICATION NUMBER: US/11/102,621
CURRENT PILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: US/10/822,300
PRIOR FILING DATE: 2004-04-09
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Pred. No. 2.8e-132;
3; Mismatches 4;
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PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/267,211
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PSECSED FOR WINDOWS VERSION 3.0
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
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Best Local Similarity 97.9%;
Matches 323; Conservative
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US-11-165-141-15
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ORGANISM: Homo sapiens
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    241 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                               Sequence 1, Application US/11075351
| Bublication No. US20050260716A1
| GENERAL INFORMATION:
| APPLICANT: Moore, Margaret D. APPLICANT: Fox, Brian A. |
| TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS TITLE OF INVENTION: DIMERIC FUSION PROTEING THEM FILE REFERENCE: 02-16
| CURRENT APPLICATION NUMBER: US/11/075,351
| CURRENT PILING DATE: 2005-03-08
| NUMBER OF SEQ ID NOS: 63
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO! 330
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PUDLication No. US20050266485A1
GENERAL INFORMATION:
APPLICANT: Fresnell, Scott R.
APPLICANT: Novak, Julia E.
APPLICANT: Novak, Julia E.
APPLICANT: Novak, Julia E.
APPLICANT: Withmore, Theodore E.
APPLICANT: Grant, Francis J.
ITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE RPERENCE: 00-108
CURRENT APPLICATION NUMBER: US/11/165,141
CURRENT APPLICATION NUMBER: US/9195,898
PRIOR FILING DATE: 2001-11-28
                                                                      301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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US-11-075-351-1
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GENERAL INFURANTION:
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: MER-131
CURRENT APPLICATION NUMBER: US/11/005,726
CURRENT FILING DATE: 2004-12-07
PRIOR APPLICATION NUMBER: PCT/EP02/12566
PRIOR FILING DATE: 2002-11-11
PRIOR FILING DATE: 2001-11-12
NUMBER OF SEQ ID NOS: 165
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 164
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OOGNVFSCSVMHEALHNHYOORSLSLSPGK 330
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                                                                                                                                          ; Sequence 164, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
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Publication No. US20060024298A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Dang, Wei
APPLICANT: Bang, Wei
APPLICANT: Karki, Sher Bahadur
APPLICANT: Karki, Sher Bahadur
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ORGANISM: Artificial Sequence
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APPLICANT: Hinton, Paul R.
APPLICANT: Hinton, Paul R.
APPLICANT: Hinton, Paul R.
APPLICANT: Teurushita, Naoya
APPLICANT: Teo, J. Yun
APPLICANT: Teo, J. Yun
APPLICANT: Vasquez, Maximilliano
APPLICANT: Vasquez, Maximilliano
APPLICANT: Vasquez, Maximilliano
APPLICANT: Vasquez, Maximilliano
TITLE OF INVENTION: ANTHRONIES BY MUTAGENESIS
FILE REFERENCE: 05882-0039-00PC03
FURBERT PALICATION NUMBER: US/11/102,621
CURRENT PILING DATE: 2006-04-08
PRIOR FILING DATE: 2006-04-09
NUMBER OF SEQ ID NOS: 146
SOPTWARE: Patentin version 3.2
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Pred. No. 2.8e-132;
3; Mismatches 4;
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; Publication No. US20050276799A1
; GENERAL INFORMATION:
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Best Local Similarity 97.9%;
Matches 323; Conservative
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LENGTH: 330
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US-11-102-621-7
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APPLICANT: Zauderer, Maurice
APPLICANT: Zauderer, Maurice
APPLICANT: Zauderer, Mark
TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
TITLE REFERENCE: 1843.0230001
CURRENT APPLICATION NUMBER: US/11/024,251
CURRENT FILING DATE: 2004-12-29
PRIOR APPLICATION NUMBER: 60/533,241
PRIOR PILING DATE: 2003-12-31
WUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.3
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                                                                                                                       , NAME/KEY: misc feature
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-11-233-683-1
                                                                                                                                                                                                                          Score 1729; DB 7;
Pred. No. 2.8e-132;
3; Mismatches 4;
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Publication No. US20050266425A1
GENERAL INFORMATION:
                                                                                                                                                                                                                       Query Match 98.0%;
Best Local Similarity 97.9%;
Matches 323; Conservative
                     LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
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SEQ ID NO 1
                                                                                                  FEATURE:
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Publication No. US20060025573A1
GENERAL INFORMATION.
APPLICANT: Gillies, Stephen
TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
FILE REFERENCE: LEX-017
CURRENT APPLICATION NUMBER: US/11/233,683
CURRENT FILING DATE: 2005-09-23
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.0
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Pred. No. 2.8e-132;
3; Mismatches 4;
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          TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILE REPERENCE: A-71306-9
CURRENT APPLICATION NUMBER: US/11/124,620
CURRENT FILING DATE: 2005-05-05
RIOR APPLICATION NUMBER: US 60/568,440
RRIOR APPLICATION NUMBER: US 60/568,440
RRIOR FILING DATE: 2004-07-15
RRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-11-09
RRIOR FILING DATE: 2004-11-09
RRIOR FILING DATE: 2004-11-09
RRIOR FILING DATE: 2004-11-10
RRIOR FILING DATE: 2004-11-10
RRIOR FILING DATE: 2004-11-10
RRIOR FILING DATE: 2004-11-10
RRIOR APPLICATION NUMBER: US 60/626,991
RRIOR PRILING DATE: 2004-11-12
RRIOR APPLICATION NUMBER: US 10/672,231
RRIOR PRILING DATE: 2004-03-26
RRIOR FILING DATE: 2004-03-26
RRIOR FILING DATE: 2003-09-26
RRIOR RPLING DATE: 2003-09-26
RRIOR RPLING DATE: 2003-09-26
RRIOR RPLING DATE: 2003-09-36
RRIOR FILING DATE: 2003-09-36
RRIOR FILING DATE: 2003-09-36
RRIOR RELING DATE: 2003-09-36
RRIOR RELING DATE: 2003-09-36
RRIOR RELING DATE: 2003-09-36
RRIOR RELING DATE: 2003-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PRECENTIN VERSION 3.3
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Best Local Similarity 97.9%;
Matches 323; Conservative
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US-11-233-683-1
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LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFPLYSKLTVDKSRW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Humanised OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                       JETIMENT APPLICATION US/11173969

Sequence 6, Application US/11173969

Publication No. US2005027167241

GENERAL INFORMATION:
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
FILE REFERENCE: 1/1211

CURRENT APPLICATION UNMBER: US/11/173,969

CURRENT FILING DATE: 2005-07-01

PRIOR PELICATION NUMBER: US/10/150,475

PRIOR PELICATION NUMBER: US/002-05-17

PRIOR PELICATION NUMBER: US/002-05-17

PRIOR PILING DATE: 2002-05-17

PRIOR PILING DATE: 2002-05-17

PRIOR PILING DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1729; DB 7; Length 4
Pred. No. 4e-132;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 161, Application US/11005726
; Publication No. US20060018903A1
GENERAL INFORMATION:
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: HELLENDOORN, TOEN
; TITLE OF INVENTION: TOF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-13
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/45,146
; PRIOR PLILING DATE: 2004-05-10
; PRIOR PLILING DATE: 2004-05-10
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                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative
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                       STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDE
     PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                               STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain US-11-172-320-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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                                                                                                                                                                                                                                                       306 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 335
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                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6, Application US/11172320
; Publication No. US20050244413A1
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Matches 323; Conservative
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                                                                                                                                                                                 0; Gaps
                                                                                                                    ) OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain US-11-005-726-161
                                                                                                                                                       Query Match 98.0%; Score 1729; DB 7; Length 450; Best Local Similarity 97.9%; Pred. No. 4.1e-132; Matches 323; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: EP 01126858.8
PRIOR FILING DATE: 2001-11-12
NUMBER OF SEQ ID NOS: 165
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 161
LENGTH: 450
                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Search completed: February 22, 2006, 22:03:44 Job time : 19.0984 secs The second secon

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

- protein search, using sw model OM protein February 22, 2006, 21:31:15; Search time 23.6408 Seconds (without alignments) 944.229 Million cell updates/sec Run on:

US-10-000-439-3 1260 Title: Perfect score:

1 EPKSCDKTHTCPPCPAPELL.......MHEALHNHYQQRSLSLSPGK 232 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	1225	97.2	:	-	GHHU	Ig gamma-1 chain C
7	1219	96.7		~	869339	ᇁ
e	1217	9.96		4	S31866	Ig gamma-1 chain C
4	1172	93.0	234	~	PT0207	,,,
co	1138	90.3		N	A23511	Ig gamma-3 chain C
ø	1136	90.2		~	A60764	Iq qamma-3 chain C
7	1123	89.1		н	G3HUWI	
œ	1107	87.9		-	G2HU	
σ	1097	87.1		ч	G4HU	
10	883	70.1		Н	GHRB	-5
11	868.5	68.9	328	N	147160	Ig gamma 2b chain
12	868.5	68.9		~	147159	Ig gamma 2a chain
13	865	68.7		~	147162	O
14	858	68.1		-	G2GP	
15	847.5	67.3		~	147158	Ig gamma 1 chain c
16	840.5	66.7		~	147161	Ig gamma 3 chain c
17	820	65.1		N	S22080	Ig heavy chain pre
18	813	64.5		N	PS0018	Ig gamma-2b chain
19	•	64.5		-	G3MSC	Ig gamma-3 chain C
20		64.4		N	C30554	بد
21		64.4		~	S31459	Ig gamma-1 chain -
22	801.5	63.6		Н	G3MSM	Ig gamma-3 chain C
23	794.5	63.1		~	PC4436	monoclonal antibod
24	789.5	62.7		ч	GIMS	Ig gamma-1 chain C
25	784.5	62.3		N	PS0017	gamma-1
56	784.5	62.3		Н	GIMSM	Ig gamma-1 chain C
27	776.5			~	S00847	gamma-2c
28	176	61.6	330	Н	G2MSA	
29	176	61.6	469	0	S37483	датта-2а

Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma heavy cha	Ig heavy chain WHI	Ig heavy chain V-I	Ig gamma-1 chain C	Ig Y heavy chain (Ig heavy chain pre	Ig mu chain C regi	Ig mu chain C regi
G2MSAB	G2MSAM	S40295	G2MS11	PS0019	GZMSBM	806611	S01321	146732	S69340	A36040	S14236	B46529	S04845	\$25644	MHMS
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335	399	446	474	322	405	327	475	180	249	218	152	572	549	343	455
61.3	61.2	60.4	59.6	59.3	59.2	58.3	58.1	53.1	43.6	43.4	43.0	29.1	28.3	28.0	28.0
772	771	761	751.5	747.5	746.5	735	731.5	699	549	547	542	366.5	357	353	353
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Tig gamma-1 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Jan-1981 #sequence. Said Results Sides (man) Species: Homo Sides Sid

A; Molecule type: DNA A; Residues: 1-330 <ELL>

A;Cross-references: UNIPROT:P01857; UNIPARC:UP10000034COE; EMBL:217370 A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, A;Note: Lys-330 is removed after translation

RiHarris, L.J.

Submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S3861

A;Molecule type: DNA

A;Residues: 2-330 c4ARA

A;Cross-references: UNIPARC:UPIO00013C6FE; EMBL:Z17370

B;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a A;Reference number: S33887; MUID:83001943; PMID:6811139

A; Noceule type: DNA
A; Residues: 88-113;235-330 < TAK>
A; Residues: 88-113;335-330 < TAK>
A; Cross-references: UNIPARC:UP1000017378B; UNIPARC:UP1000017378C; EMBL:Z17370
B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B; Cunningham, B.A.; Rutishauser, U.; Amino acid sequer
A; Reference number: A90563; MUID:71064024; PMID:5489771
A; Contents: myoloma protein Bu
A; Residues: protein
A; Residues: 1-56, R.; 98-135 < CUNN
A; R.; 98-135 < CUNN
A; R.; 98-135 < CUNN
A; 98-135 <

A; Accession: A90564

A;Molecule type: protein
A;Rosidues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Cross-references: UNIPARC:UP1000017378E
A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H; Hilschmann, N.

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Ig gamma-1 chain C region - synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: S72664
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-140,'C',
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A, Residues: 1-96, 'R', 99-197, 'D', 199-218, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A, Residues: 1-96, 'R', 99-197, 'D', 199-218, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A, Roce: this sequence has the Glm(3) and Glm(non-1) markers
B, Gall, W.E.; Edelman, G.M.
B, Gall, W.E.; Edelman, G.M.
A, 118-1196, 1376, 1370
A, Thle: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfic
A, Reference number: A90565; MUID: 71064027; PMID: 4923144
A, Contents: annotation; disulfide bonds
B, Decker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A, Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A, Title: Rule of antibody structure. The primary structure of monoclonal igG1 immunoglob
A, Reference number: A91667; MUID: 77070267; PMID: 1002129
A, Contents: annotation; disulfide bonds
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Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie).
igen Primaerstruktur.
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A;Introns: 99/1; 114/1; 224/1
A;Introns: 1 mmunoglobulin c region; 1mmunoglobulin homology
C;Keywords: duplication; 91ycoprotein; heterotetramer; immunoglobulin
F;137-206/Domain: immunoglobulin homology <IM2>
F;20-85/Domain: immunoglobulin homology <IM3>
F;21-310/Domain: immunoglobulin homology <IM3>
F;21-310/Domain: immunoglobulin homology <IM3>
F;21-310/Domain: immunoglobulin homology <IM3>
F;10-310/Domain: immunoglobuli
                                                                                                                                                                                                                                                                     A, Molecule type: protein
A, Residues: 1-34'O', 36-96'K', 98-115,'Q', 117-197,'D', 199-238,'D', 240,'L', 242-268,'E',
A; Cross references: UNIPARC: UPI000017378F
A; Note: this sequence has the Gim(1) and Gim(1) markers
A; Note: this sequence has the Gim(1) and Gim(1) Markers
B; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 FA; Reference number: A91723; MUD: 83289131; PMID: 6884994
A; Contents: myeloma protein KOL; disulfide bonds
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                                                                                                                                        A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contente: myeloma protein Nie
A;Accession: B91668
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A,Cross-references: GDB:120085; OMIM:147100
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Best Local
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Ig heavy chain V region precursor - human C; Species: Homo sapiens (man)

RESULT 2 S69339

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C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: 831866
R;Filpula, D.
B;Dilpula, D.
A;Filpula, D.
A;Filpula, D.
A;Filpula, D.
A;Filpula, D.
A;Reference number: S31866
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000 C;Accession: $69339; $72664  
R;Khamlich!, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M. Bicchem. 229, 54-60, 1995  
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A;Reference number: $69339; MUID:95262687; PMID:7744049  
A;Accession: $69339  
A;Accession: $69339  
A;Accession: $69339  
A;Accession: $69339  
A;Cessidues: preliminary A;Molecule type: mRNA A;Residues: 1-374  
A;Accession: $68339  
A;Crose-references: UNIPARC:UP10000176F24; EMBL:X81695  
B;Khamlichi, A.A.  
Submitted to the EMBL Data Library, September 1994
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A;Molecule type: mRNA
A;Residues: 1-255 <FILD-
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068;
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
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A;Cross-references: UNIPARC:UP1000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Pred. No. 4.9e-85;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
96.7%; Score 1219; DB 2;
Best Local Similarity 96.1%; Pred. No. 5.5e-85;
Matches 223; Conservative 5; Mismatches 4;
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Ug gamma-3 heavy chain disease proteins - human CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiDate: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999 CiAccession: A90442; A9219; A90198; A93915; A02149 R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C. Bicchemistry 19, 4304-4308, 1980 A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A;Contents: heavy chain disease protein Wis A;Contents: heavy chain disease protein Wis A;Contents and A90442 A;Molecule type: protein A;Residues: 1-289 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         u) with an IGHG4 conver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiems (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IA;Reference number: A60764; MUID:90007613; PMID:2571587
A;Reference number: A60764
                                                                                             146 BPKSCDTPPPCPRCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQP
                                                                                                                                                                                                                                 206 KWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                    266 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP
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                                                                 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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   13; Indels
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C;Superfamily: immunoglobulin homology
C;Keyworde: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1136; DB 2;
; Pred. No. 1.1e-78;
11; Mismatches 13;
   11; Mismatches
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Best Local Similarity 89.7%;
Matches 208; Conservative 1:
   208; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
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      Matches
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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: CA;Recession: A23511; MUD:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Genetics:
A;Geneti
                                                                                                                                                                                                                                                                                                                                                   Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;State: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: P70207
C;Accession: P70207
C;Accession: P70207
C;Accession: P70207
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: P70207
A;Molecule type: mRNA
A;Residues: 1-234 <ERR>
A;Accession: P70207
A;Molecule type: mRNA
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>F;48-117/Domain: immunoglobulin homology <IMM>F;48-117/Domain: immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                      1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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89.7%; Pred. No. 7.5e-79;
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Best Local Similarity
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A; Molecule type: DNA
A; Residues: 1-326 < ELL.)
A; Residues: 1-326 < ELL.)
A; Croses-references: UNIPROT: P01859; UNIPARC: UPI000003BFCC; GB: V00554; GB: J00230; NID: g3.
A; Note: Lys-326 is probably removed posttranslationally
B; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
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C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l C; Complex: An immunoglobulin C region; immunoglobulin homology
C; Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85, Domain: immunoglobulin homology < IMI>
F; 239-306, Domain: immunoglobulin homology < IMI>
F; 239-306, Domain: immunoglobulin homology < IMI>
F; 244, Disulfide bonds: interchain (to light chain) #status experimental
F; 27-33, 140-200, 246-304/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A; Residues: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A; Cross-references: UNIPARC: UPI0000173792; UNIPARC: UPI0000173793
A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.M.
R; Hofmann, T.; Parr, D.M.
A; Hofmann, T.; Parr, D.M.
A; Hote on the amino acid sequence of residues 381-391 of human immunoglobulin and the sequence of residues and the sequence of the sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Reference number: A9451
A,Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A,Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 < WAN>
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 < WAN>
A;Roose-references: UNIPARC:UP10000173791
A;Note: Trp-156 is at or near the complement-binding site
A;Onnell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Ritle: The amino acid sequences of the three heavy chain constant region domains of A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
                                                human immunoglobulin G2
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immu A;Federane number: A90533; WIDD: 22033500; PWID: 440472
A;Contents: annotation; myeloma protein Sa, disulfide bonds R;Frangione, B.; Milstein, C.; Pink, J.R.L.
A;Title: Structural studies of immunoglobulin G.
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MID: 69064124; PMID: 5782707
A;Contents: annotation; Sa, disulfide bonds
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A,Gene: GDB:IGHG2
A,Cross-references: GDB:119338; OMIM:147110
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A,Residues: 238-275 <HOF>
A,Cross-references: UNIPARC:UPI0000173794
R,Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
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A, Cross-references: UNIPARC: UPI0000173797
A, Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain a, Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cc A, Note: the sequence of residues 42-76 was taken from the reference that follows R, Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A, fittle: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication A, Reference number: A92219; MUID: 77118561; PMID:402363
A, Coccession: A92219
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A/RCCHOBLOOL 1790: MRNA
A/RCGEDILE trype: mRNA
C/RCGEDILE trype: mR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        idue segment (12-28)
A;Note: Cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form intex
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A;Accession: A90198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 59-125, EB: 1.128-226, 228-289 < WOL>
A; Residues: 59-125, EB: 1.128-226, 228-289 < WOL>
A; Cross-references: UNIPARC: UDIO000173799
A; Note: this protein lacks most of the V region, all of the CH1 region, and part of the R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.; Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion A; Reference number: A93915; MUID: 82247835; PMID: 6808505
A; Contents: heavy chain disease protein Omm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Reaidues: 12-97 kMIC-
A;Reaidues: UNIPARC:UP10000173798
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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88.3%; Pred. No. 7.5e-78;
iive 14; Mismatches 13
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Matches 204; Conservative
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Length 326;

87.9%; Score 1107; DB 1;

Query Match

Ig gamma-2 chain C region - hu C;Species: Homo sapiens (man)

G2HD

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Ig gamma chain C region - rabbit
Cispecies: Oxyctolagus cuniculus (domestic rabbit)
Cjate: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
CjAccession: A91749; A90290; A33928; A90245; A94416; A02Ī61
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Rmunogenerics 18, 387-397, 1981
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplo.
A;Reference number: A91749; MUID:84030930; PMID:6313520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-323 <BER>
A; Cross-references: UNIPROT: P01870; UNIPARC: UPI000012B37D
A; Cross-references: UniPROT: P01870; UNIPARC: UPI000012B37D
A; Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
B; Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A; Title: Sequence studies on the constant region of the Fd sections of rabbit immunogloi
A; Reference number: A90290; MUID: 76135469; PMID: 1243651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A;Residues: 1-47, E', 49-71, PV', 72-128 <PRA>
A;Residues: 1-47, E', 49-71, PV', 72-128 <PRA>
A;Cross-references: UNIPARC:UP1000173AB
B;Across-references: UNIPARC:UP1000173AB
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy Chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A;Reference number: A93928; MUID:83299917; PMID:6193512
A;Accession: A93928
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A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Cross=references: Unitabac:up100010652Eb; GB:M16426; UID:9165111; PIDN:AAA31289.1; PID
A; Note: this sequence has the dil allotypic marker, 104-Met, and the e15 allotypic mark-
B; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A; Title: Sequence studies of the FG section of the heavy chain of rabbit immunoglobulin
A; Reference number: A90245; MUID:70110015; PMID:5461106
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A; Residues: 132-143, E', 45-161 < FRU>
A; Residues: 132-143, E', 45-161 < FRU>
A; Cross-references: UNIPARC: UP10000137AC
B; Hill, R.L.; Lebovitz, H.B.; Pellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A; Reference number: A94416
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A Mesidual Eype: Drotein
A Mesidual Eype: Drotein
A Mesidual Eype: 129-172, D., 174-184, A., 186, E., 188-200, D., 202-217, E., 219-232, 'Q', A. Mesidual Experiment Eype: Drotoin Eyper 
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                                                226 PQVYTLPPSQBEMTKNQVSLTCLVKGFYPSDIAVEWBSNGQPENNYKTTPPVLDSDGSFF 285
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F;236-303/Domain: immunoglobulin homology <1M3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                            LYSRLIVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327
                                                                                                                                                                                            LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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; Pred. No. 1.3e-59;
34; Mismatches 38.
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64.5%;
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Best Local Similarity
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Gypamma-4 chain C region - human

Gypacies: Homo sapiens (man)

Cypacies: Homo sapiens (man)

A,Trilles Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A,Trilles Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A,Trilles Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A,Trilles Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A,Reference number: A90933

A,Molecule type: DNA

A,Reference number: A90933

A,Molecule type: DNA

A,Trilles Human immunoglobulin sublclasses. Partial amino acid sequence of the constant x

A,Trille: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant x

A,Reference number: A90249

A,Trille: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant x

A,Reference number: A90249

A,Trille: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant x

A,Reference number: A90249

A,Tross-references: UNIPARC:UP10000173795; UNIPARC:UP10000173796

C,Complex: An immunoglobulin heteroteramer subunit consists of two identical light (kap)

A,Tross-references: UNIPARC:UP10000173795; UNIPARC:UP1000173796

C,Complex: An immunoglobulin heteroteramer subunit consists of two identical into la

C,Superfamily: immunoglobulin homology cluz>

F,194-196/Nomain: immunoglobulin homology cluz>

F,194/Disulfide bonds: interchain (to light chain) #F10/Disulfide 
                                                         'n
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                                                                                                                                                                                                                                                                                                                                                                               99 ERKCCVE---CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 274
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F;240-303/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                            1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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87.1%; Score 1097; DB 1; Length 327;
Best Local Similarity 90.5%; Pred. No. 8.1e-76;
Matches 201; Conservative 11; Mismatches 10; Indels (
                                                     Indels
    No. 1.4e-76;
smatches 11;
                                                205; Conservative 12; Mismatches
         88.4%; Pred.
Best Local Similarity
Matches 205; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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A;Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:g433123; PIDN:AAA52217.1; P:C;Genetics:
C;Genetics:
A;Gene: 1992a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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Matches 158; Conservative
                                                                                                                        Query Match
Best Local Si
Matches 157;
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Best Local S
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A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:g433125; PIDN:AAA52218.1;
C;Genetics:
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C;Species: Sus scrota domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 356-3573, 1994
A;Itle: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147159; MUID:95015845; PMID:7930579
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Cjopecies: Sus scrofts domestics (domestic pig)
Cjobecies: Sus scrofts domestics (domestic pig)
Cjobete: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
Cjocession: 147160
R,Kacsbkovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the CDNA sequences A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147160
A;Accession: 147160
A;Accession: GB/EMBL/DDBJ
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                                                                                                                         EWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQR 224
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                                                                                                                                                                                                                                                                                                                                                                                         gamma 2b chain constant region - pig (fragment)
Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                               TCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEY
                                                                                                        KCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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Matches 157;
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A;Cross-references: UNIPARC:UPI0000115527; EMBL:U03782; NID:g433129; PIDN:AAA52220.1; 1
C;Genetics:
A;Gene: 1gG4
A;Gene: 1gG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
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Ig gamma 4 chain constant region - pig (fragment)
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: I47162
R;KacsKovics, I; Susu, J; Butler, J.E.
R;KacsKovics, I; Susu, J; Butler, J.E.
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: I-277 <KAC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 GOTREPOVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWQRNGOPEPEGNYRTTPPQQ 228
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C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                          49 TXTKPPCPICPACEGPGPSAFIFPPKFKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVD
                                                                                                                                                                                                                                                                                                                                                                                         71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE
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                                                                                                                                                                                            CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
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                                                                                              Gaps
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    Length 328;
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                                                                                              Indels
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/ Match 68.9%; Score 868.5; DB 2; Local Similarity 70.1%; Pred. No. 1.6e-58; Les 157; Conservative 32; Mismatches 32;
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69.0%; Pred. No. 2.5e-58;
ive 32; Mismatches 35;
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RESULT 15
147158
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15 gamma 1 chain constant region - pig (fragment)
C; Species: Sus ecrofa domestica (domestic pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Accession: 147158
B; Kaccestovica, I.; Sun, U.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A; Accession: 147158
A; MUD:95015845; PMID:7930579
A; Accession: 147158
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-328 «KAC>
A; Residues: 1-328 «KAC>
A; Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:9433121; PIDN:AAA52216.1; P
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163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 HTAETRPKEEQFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
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                                                                                                                                      277 TPPIEDADGSYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: 1gG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
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Matches 156; Conservative
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F;241-310/Domain: immunoglobulin homology <IM3>
F;241-310/Domain: immunoglobulin homology <IM3>
F;241-310/Domain: immunoglobulin homology <IM3>
F;242-202/Disulfide bonds: #status experimental
F;142-202/Disulfide carbohydrate (Asn) (Covalent) #status experimental
F;148/Binding site: carbohydrate (Asn) (Covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental
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Accession: A94553; A90352; A90359; A90384; A90385; A02151
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                                                      February 22, 2006, 21:37:34; Search time 34.4594 Seconds
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1 BPKSCDKTHTCPPCPAPELL.......MHRALHNHYQQRSLSLSPGK 232
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       GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-178-869-2
US-09-761-413-2
US-09-949-713-11
US-08-26-311-7
US-08-457-918-7
US-10-157-408-7
US-09-949-713-22
US-09-949-713-22
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PCT-US96-10043-11
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US-08-397-411-7
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US-08-030-175-42
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US-09-176-228-3
                                                                                                                                            572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 31-JAN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CAREOLL, PETR G.

REGISTRATION NUMBER: 32,837

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: SGAR-00371

TELEPHONE: (415) 705-8410

TELEPHONE: (415) 705-8410

INFORMATION FOR SEQ 1D NO: 50:
                                                                                                                                                                                                                                                                                                                                                                    US-08-555-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTCOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1225; DB 1;
Pred. No. 3.5e-116;
3; Mismatches 4;
US-10-104-047-3730
US-08-740-002-27
US-08-487-550-10
US-08-487-550-12
US-09-526-098-4
US-09-526-098-12
US-09-383-916-12
US-09-383-916-12
US-09-758-173-14
US-09-758-173-14
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US-09-576-098-8
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US-09-576-928-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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97.0%;
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Best Local Similarity 97.0
Matches 225; Conservative
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MOLECULE TYPE: protein
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160 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 219
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                                                                                                                                                                                                                         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                            100 EPRSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKF
                                                                                                                                                1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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Patent No. 6197294

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hickey, William F

APPLICANT: Hackey, William F

APPLICANT: Baetge, E. Edward

TILLE OF INVENTION CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043

CURRENT APPLICANT: 1998-10-26

UURBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 14
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Length 232;
                                                       Indels
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Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 3.5e-116; Matches 225; Conservative 3; Mismatches 4;
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97.0%; Pred. No. 5.9e-116;
iive 3; Mismatches 4;
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APPLICANT: Tao, Weng
APPLICANT: Wong, Shou
APPLICANT: Hickey, William F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 97.0 Matches 225; Conservative
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ORGANISM: Homo sapiens
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US-09-178-869-2
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Sequence 26, Application increased increa
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US-09-32-812A-26
US-09-32-812A-26
US-09-32-812A-26

Patent No. 6906292
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Increased biological
TITLE OF INVENTION: activities
TITLE OF INVENTION: activities
TITLE OF INVENTION: activities
CURRENT APPLICATION UNMER: US/09/932,812A
CURRENT APPLICATION UNMER: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
TANDER: 202
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US-09-968-362A-26
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Sequence 7, Application US/08236311;
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Grapory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-949-713-11
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US-08-236-311-7
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            APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/761,413
CURRENT FILING DATE: 2001-01-16
PRIOR PAPLICATION NUMBER: US/09/178,869
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                              Length 331;
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| Patent No. 6306395
| GENERAL INFORMATION:
| APPLICANT: NAKAWIRA, No. 630639510
| TITLE OF INVENTION: NOVEL FAB ANTIGEN DERIVATIVE
| TITLE OF INVENTION: NOVEL FAB ANTIGEN DERIVATIVE
| CURRENT FILING DATE: 1990-105.
| CURRENT FILING DATE: 1997-05-01
| EARLIER FILING DATE: 1997-05-01
| NUMBER OF SEQ ID NOS: 25
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 11
| LENGTH: 360
| TYPE: PRT
| CORGANISM: Homo sapiens
| US-09-180-100-11
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Hammang, Joseph P.
                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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US-09-180-100-11
                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 331
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232
                            309 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSBGK 360
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                                                                                                                                                                          Sequence 11, Application US/09949713
; Sequence 11, Application US/09949713
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: NAKAWURA, No. 6953847io
; APPLICANT: NAKAWURA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR FILING DATE: 1998-11-02
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11

LEMETH: 360
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Pred. No. 6.6e-116;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATIN GENERICACH)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
97.2%; Score 1225; D
Best Local Similarity 97.0%; Pred. No. 6.6e
Matches 225; Conservative 3; Mismatches
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121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 371;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 6.9e-116; Matches 225; Conservative 3; Mismatches 4;
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Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P0444P1C3
             FILING DATE: 1. JOUR-1973
FILING DATE: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/236311
PILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 36/575
REFERENCE/DOCKET NUMBER: 36/575
REFERENCE/DOCKET NUMBER: 36/575
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: 415/225-8828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-157-408-7; Sequence 7, Application US/10157408; Patent No. 6710169; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 amino acids
1-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-457-918-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.2%; Score 1225; DB 1; Length 371; 97.0%; Pred. No. 6.9e-116; tive 3; Mismatches 4; Indels
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         FILLING DALES:

CLASSIFICATION: 2. ....

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 07/84277

FILING DATE: 18-FEB-1992

PRIOR APPLICATION NUMBER: 07/84277

FILING DATE: 18-FEB-1992

PRIOR APPLICATION NUMBER: 07/104329

FILING DATE: 28-SEP-1988

PRIOR APPLICATION NUMBER: 07/104329

FILING DATE: 28-SEP-1986

PRIOR APPLICATION NUMBER: 28,616

REPIERSON NUMBER: 28,616

REGISTRATION NUMBER: 28,616

REPERENCE/DOCKET NUMBER: 28,61
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APPLICANT: Capon, Daniel J.
APPLICANT: Gagory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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Patent No. 6117655
      02-MAY-1994
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Best Local Similarity 97.04
Matches 225; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inc
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145 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 204
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                                                                                                                                                                                                                                                                                             205 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                      1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                      Length 376;
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; Patent No. 6953847
; Fatent No. 6953847
; GENERAL INFORMATION:
; APPLICANT: NAKAWIRA, No. 695384710
; APPLICANT: NAKAWIRA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT FILING DAPE: 2001-09-12
; PRIOR PLING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR APPLICATION NUMBER: POT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIN Ver. 2.0
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                                                                      Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 7.1e-116; Matches 225; Conservative 3; Mismatches 4;
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97.0%; Pred. No. 7.1e-116;
tive 3; Mismatches 4;
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US-10-679-999-9
'Sequence 9, Application US/10679999
'Patent No. 6936439
'GENERAL INFORMATION:
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Best Local Similarity 97.0<sup>†</sup>
Matches 225; Conservative
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     ORGANISM: Homo sapiens
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                 us-09-180-100-22
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Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMINA, No. 6306395io
APPLICANT: NAKAMINA, No. 6306395io
APPLICANT: NAKAMINA, No. 6306395io
APPLICANT: NAKAMINA, No. 6306395io
FILE REFERENCE: 1110-207P;
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1999-05-01
NUMBER OF SEQ ID NOS: 25
SEQ ID NOS: 25
SEQ ID NO 22
LENGTH: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                            PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
APPLICATION NUMBER: 08/33311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/84277
FILING DATE: 28-EP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 28-EP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 28-EP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 38-EP-1987
ATTORNEY/AGENT INFORMATION:
NAME: KUDINGC, JEffery S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: 90444PIC3
TELECOMMUNICATION: 1415/25-8228
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,408
FILING DATE: 28-May-2002
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-157-408-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 371 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS
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US-09-176-228-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 121
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            Hecht, Randy I.
TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1
OTHER INFORMATION: /note= "Met (ATG) starts at SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                               COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/679,999
FILING DATE: 06-0cc-2003
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/568,528
FILING DATE: 09-May-2000
APPLICATION NUMBER: 09/267,517
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                          NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
STREET: 1840 DeHavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Knight, Matthew W.
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: A-416
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 379 amino acida
TYPE: amino acid
STRANDEDNESS: unknown
APPLICANT: Mann, Michael B.
                                                                                                                                                            CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.0
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-679-999-9
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Sequence 3, Application US/08784512 Patent No. 5872209 GENERAL INFORMATION: APPLICANT: BARTNIK, Eckart APPLICANT: BIDENWIELLER, Bernd APPLICANT: BUETTWER, Frank

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APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: and native aggreean to study the proteolytic activity of
TITLE OF INVENTION: "Aggrecanase" in cell culture systems
NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96100682.2
APPLICATION NUMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANDOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.2%; Score 1225; DB 1; Best Local Similarity 97.0%; Pred. No. 7.6e-116; Matches 225; Conservative 3; Mismatches 4;
                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09176228
Patent No. 618034
GENERAL INFORMATION:
APPLICANT: BARTNIK, Eckart
APPLICANT: BIGHTMELER, Bernd
APPLICANT: RIDENMUELLER, Bernd
APPLICANT: CATERSON, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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; LOCATION: 1..396
US-08-784-512-3
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APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: "Aggrecanase" in cell culture systems
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLGY & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
CUNTRY: USA
COUNTRY: USA
COUNTRY: USA
SITE 1000 FOR COMPATION BATH
COUNTRY: USA
COMPUTER: IBW PC-COMPATION BATH
MEDIUM TYPE: Floppy disk
COMPUTER: RADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: USA
COMPUTER: USA
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/176,228
FILING DATE: 18 -JAN-1996
ATTORNEY/AGRATI INFORMATION:
PRESERRANCE/OCKET NUMBER: 18 -JAN-1996
ATTORNEY/AGRATI INFORMATION:
REGISTRATION NUMBER: 33,683
RESERRANCE/OCKET NUMBER: 18 -JAN-1997
APPLICATION NUMBER: 18 -JAN-1996
ATTORNEY/AGRATI INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 22, 2006, 21:39:49 Job time : 35.4594 secs
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein i LOCATION: 1..396 US-09-176-228-3
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Conservative
; ORGANISM: Homo sapiens US-09-847-208-3
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Query Match
Best Local S
Matches 232
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7, Appli
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Sequence 29,
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1 EPKSCDKTHTCPPCPAPELL.......MHEALHNHYQQRSLSLSPGK 232
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              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-647-208-2

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US-10-066-673-29

US-10-966-673-19

US-10-966-673-19

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Sequence 8,
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| Publication No. US20030082190A1
| GENERAL INFORMATION:
| APPLICANT: Saxon, Andrew
| APPLICANT: Zhang, Ke
| APPLICANT: Zhu, Daocheng MOLECULES AND TREATMENT OF
| TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
| TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
| TITLE OF INVENTION: 19E-MEDIATED ALLERGIC DISEASES
| FILE REPERENCE: UC67.002A
| CURRENT APPLICATION NUMBER: US/09/847,208
| CURRENT APPLICATION NUMBER: 201-05-01
| NUMBER OF SEQ ID NOS: 177
| SEQ ID NO 3
| SEQ ID NO 3
| LENGTH: 232
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US-10-000-439-3
Sequence 3, Application US/10000439
Publication No. US20030064063A1
GENERAL INFORMATION:
APPLICANT: SAXON, Andrew
TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
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100.0%; Pred. No. 1.1e-92;
ive 0; Mismatches 0;
US-09-822-851B-14
US-10-119-637A-14
US-11-129-083-14
US-11-129-083-14
US-11-129-080-14
US-11-129-080-14
US-11-129-080-14
US-10-129-095-898A-15
US-09-995-898A-15
US-09-995-898A-15
US-10-047-542-20
US-10-047-542-20
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US-10-12582-1
US-10-1383-902A-81
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219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
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   279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Publication No. US20030082190A1

GENERAL INPORMATION:
APPLICANT: Stang, Ke

APPLICANT: Zhang, Ke

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 177

SOFTWARE: FREESE FREES FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREE
                                                                                                                                            Sequence 2, Application US/10000439; bublication No. US20030064063A1; bublication No. US20030064063A1; general inpormation:
    APPLICANT: Saxon, Andrew
    TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES; FILE REFERENCE: UCO67.004A A; CURRENT FAPLICATION NUMBER: US/10/000,439; CURRENT FILING DATE: 2001-10-24; PRIOR APPLICATION NUMBER: US 09/847,208; PRIOR APPLICATION NUMBER: US 09/847,208; PRIOR FILING DATE: 2001-05-01; NUMBER OF SEQ ID NOS: 13; SOFTWARE: FRRESQ for Windows Version 4.0
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100.0%; Pred. No. 1.7e-92;
tive 0; Mismatches 0;
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COTHER INFORMATION:
US-09-847-208-7
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TYPE: PRT
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LENGTH: 569
                                                                                                                                     JS-10-000-439-2
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Publication No. US20030082190A1
GENERAL INPORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: EUS-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FREUSED FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1260; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e-92; Matches 232; Conservative 0; Mismatches 0;
FILE REFERENCE: UC067.004A
CURRENT APPLICATION NUMBER: US/10/000,439
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 09/847,208
PRIOR FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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TYPE: PRT
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Sequence 10, Application US/09996357

GENERAL INFORMATION:

APPLICANT: Getter, Malcolm L

APPLICANT: Getter, David I

APPLICANT: Geselin, Michael

APPLICANT: Goselin, Michael

TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR

TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE

TITLE OF INVENTION: TOOI-11-27

CURRENT FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-29

PRIOR PLILING DATE: 2000-11-29

PRIOR FILING DATE: 2000-11-20

WINMER OF SEQ ID NOS: 13

SOFTWARE: PatentIN Ver: 2.0
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97.0%; Pred. No. 7.1e-90;
cive 3; Mismatches 4;
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CURRENT FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: US 60/562,627
PRIOR FILING DATE: 2004-04-14
PRIOR APPLICATION NUMBER: US 60/511,687
PRIOR FILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.2
SEQ ID NO 29
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Best Local Similarity 97.04
Matches 225; Conservative
                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: HOMO SAPIENS
US-10-966-673-29
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CORGANISM: Homo sapiens
US-09-996-357-10
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US-09-996-357-10
                                                                                                                                                                                                                 LENGTH: 330
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Publication No. US20050226864A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Hinton, Paul R
APPLICANT: Tsurushita, Naoya
TILLE OF INVENTION: Alteration of Fc-Fusion Protein Serum Half-Lives By Mutagenesis
FILE REFERENCE: 05882.0039.NPUS07
CURRENT APPLICATION NUMBER: US/10/966,673
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     EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                      BPKSCDKTHTCPPCPAPELLGGBSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                   PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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APPLICANT: SAXON, ANDREW; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES; FILE REFERENCE: UC067.004A; CURRENT APPLICATION NUMBER: US/10/000,439; CURRENT FILING DATE: 2001-10-24; PRIOR FILING DATE: 2001-10-24; PRIOR FILING DATE: 2001-05-01.
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1260; DB 4; Best Local Similarity 100.0%; Pred. No. 3.2e-92; Matches 232; Conservative 0; Mismatches 0;
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TYPE: PRT
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APPLICANT: Women Scott K.
APPLICANT: Wann, Michael B.
APPLICANT: Dunstan, Colin R.
TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods FILE REFERENCE: A-604
CURRENT APPLICATION NUMBER: US/09/389,782
CURRENT FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
                                                                                   PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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Publication No. US20040110929A1
GENERAL INFORMATION:
APPLICANT: Bjorn, Soren E
APPLICANT: Bjorn, Soren E
APPLICANT: Jorgensen, Rise M
APPLICANT: Jorgensen, Anker S
TITLE OF INVENTION: TF Binding Compound
FILE REFERENCE: 6455.200-US
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: Danish Application No. PA
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-08-19
FRIOR FILING DATE: 2002-08-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
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3; Mismatches
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Publication No. US20030144187A1
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Best Local Similarity 97.0°
Matches 225; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
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US-09-389-782-1
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US-10-761-593A-26

Sequence 26, Application US/10761593A

Sequence 26, Application US/10761593A

Sequence 26, Application US/10761593A

Publication No. US20040175824A1

GENERAL INFORMATION:
APPLICANT: Sun, Bill N

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: activities
TITLE OF INVENTION: activities
FILE REPERENCE: 025UN2001-A

CURRENT PPLICATION NUMBER: US/10/761,593A

CURRENT FILING DATE: 2004-01-21

PRIOR FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.2
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97.2%; Score 1225; DB 4; Length 232; 97.0%; Pred. No. 7.1e-90;
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Pred. No. 7.1e-90;
3; Mismatches 4;
                                               3; Mismatches
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Best Local Similarity 97.0%;
Matches 225; Conservative
                          Best Local Similarity 97.0
Matches 225; Conservative
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US-10-831-622-97
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Query Match 97.2%; Score 1225; DB 5; Best Local Similarity 97.0%; Pred. No. 7.1e-90; Matches 225; Conservative 3; Mismatches 4;
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ORGANISM: Homo sapiens
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Publication No. US20040259209A1

GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill
APPLICANT: Sun, Rill
APPLICANT: Sun, Rill
APPLICANT: Sun, Reill
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fr fusion proteins of human granulocyte colony-
TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 0350N2001
CURRENT APPLICATION NUMBER: US/10/800,497
CURRENT FILING DATE: 2004-03-15
PRIOR FILING DATE: 2001-10-01
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 232
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                                                                                                                                                                                                                                                                                                                                    Length 232;
                                                                                                                                                                                                                                                                                                                                                                                Indels
APPLICANT: Wilkinson, Beverley
TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: TSRI 810.1
CURRENT APPLICATION UNMBER: US/10/831,622
CURRENT FILING DATE: 2004-04-23
PRIOR PELLING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 232
                                                                                                                                                                                                                                                                                                                                  Score 1225; DB 5;
Pred. No. 7.1e-90;
3; Mismatches 4;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 232
TYPE: PRI
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Best Local Similarity 97.0%;
Matches 225; Conservative
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US-10-831-622-97
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US-10-800-497-26
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RESULT 14
US-10-800-449-26
Sequence 26, Application US/10800449
Sequence 26, Application US/10800449
Sequence 26, Application No. U320040265973A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: increased biological activities
TITLE OF INVENTION: increased biological activities
FILE REPERENCE: 036UN2001
CURRENT APPLICATION NUMBER: US/10/800,449
CURRENT FILING DATE: 2004-03-15
PRIOR FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 232
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APPLICANT: Kaye, Jonathan
TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION
TITLE OF INVENTION: OF TRANSPLANT REJECTION
FILE REPERENCE: TSRI 810.2
CURRENT FILING DATE: 2004-10-12; PRIOR APPLICATION NUMBER: US/10/964,215
PRIOR PILING DATE: 2004-04.23; PRIOR PELICATION NUMBER: US 60/467,206; PRIOR APPLICATION NUMBER: US 60/467,206; NUMBER OF SEQ ID NOS: 113
SOFTWARE: FastERQ for Windows Version 4.0
SEQ ID NOS: 113
PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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Query Match 97.2%; Score 1225; DB 5; Length 232; Best Local Similarity 97.0%; Pred. No. 7.1e-90; Matches 225; Conservative 3; Mismatches 4; Indels (
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Search completed: February 22, 2006, 22:03:09 Job time : 119.604 Bec8

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RESULT 2
US-11-227-340-7
; Sequence 7, Application US/11227340
; Publication No. US20060024730A1
; GENERAL IRPORMATION:
; APPLICANT: Bjorn, Soren E
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                                                                   February 22, 2006, 21:58:19; Search time 12.0207 Seconds (without alignments) 287.324 Million cell updates/sec
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Sequence 161,
Sequence 701,
Sequence 7, Ag
Sequence 6, Ag
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*
GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-11-227-340-7

US-11-222-24-6

US-10-886-383-6

US-10-982-440-68

US-10-922-240-11

US-11-075-351-1

US-11-105-141-15

US-11-102-621-3

US-11-102-621-3

US-11-102-621-3

US-11-102-621-3

US-11-102-621-1

US-11-233-663-1

US-11-233-63-1

US-11-173-959-6

US-11-158-555-33

US-11-158-555-33

US-11-16-503-6

US-11-16-503-6

US-11-16-503-6

US-11-16-503-6

US-11-016-503-6

US-11-016-503-8

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Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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US-10-948-053-1
Sequence 1, Application US/10948053
Publication No. US20060019887A1
Publication No. US20060019887A1
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for the Prevention or Treatment of Cancritie Prince Programmers (Compositions)
TITLE OF INVENTION: Bone Loss Associated with Cancer TITLE OF INVENTION: WUMBER: US/10/948,053
TITLE REFERENCE: A-605
CURRENT APPLICATION NUMBER: US/10/948,053
CURRENT FILING DATE: CURRENT APPLICATION NUMBER: US/09/389,545
PRIOR APPLICATION TILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                 389, App
4, Appli
71, Appl
121, App
132, App
70, Appl
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US-11-139-499-4
US-11-139-499-12
US-11-022-289-8
US-11-022-289-8
US-11-022-289-8
US-11-022-289-6
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US-11-022-289-6
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US-11-227-340-6
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US-11-227-340-6
US-11-102-621-71
US-11-102-621-71
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Best Local Similarity 97.0
Matches 225; Conservative
    SEO ID NO 1
LENGTH: 232
TYPE: PRT
ORGANISM: Homo sapiens
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Score 1225; DB 6;
Pred. No. 2.6e-101;
3; Mismatches 4;
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; Sequence 20, Application US/10493909
; Publication No. US20060015969A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.0%;
Matches 225; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 330
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US-10-886-383-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 79
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PAPLICANT: Jorgensen, Anker S
TITLE OF INVENTION: TF Binding Compound
FILE SEPERACE: 6455.200-US
CURRENT APPLICATION NUMBER: US/11/227,340
CURRENT FILING DATE: 2005-09-15.
PRIOR APPLICATION NUMBER: US/10/617,619
PRIOR APPLICATION NUMBER: US/10/617,619
PRIOR APPLICATION NUMBER: US/002-07-11
PRIOR APPLICATION NUMBER: US 60/404,568
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-09-19
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 14
SOSTWARE: PATENTIN VERSION 3.3
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Pred. No. 1.7e-101;
3; Mismatches 4; Indels
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APPLICANT: RAKOL, Mark W.
APPLICANT: Acos, Jane A.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REFERENCE: 01-20
CURRENT APPLICATION NUMBER: US/11/242,294
CURRENT APPLICATION NUMBER: US/10/152,363
PRIOR FILING DATE: 2002-05-20
PRIOR PLING DATE: 2002-05-24
NUMBER OF SEQ IO NOS: 70
SOFTWARE: FastSEQ for Windows Version 3.0
SETUND FILING DATE: 201-05-24
NUMBER OF SEQ ID NOS: 70
SEQ ID NOS 6
LENGTH: 251
TYPE: PRI
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Pred. No. 1.9e-101;
3; Mismatches 4;
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; Sequence 6, Application US/11242294
; Publication No. US20060034852Al
; GENERAL INFORMATION:
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Best Local Similarity 97.0%;
Matches 225; Conservative 3
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Best Local Similarity 97.0%;
Matches 225; Conservative 3
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US-11-242-294-6
                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                              LENGTH: 232
                                                                                                                                                                                                                                                                                                                                   US-11-227-340-7
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                                                                                                                                                                                                                                                              SEQ ID NO 7
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Sequence Application US/10886383

Publication No. US20060005571A1

GENERAL INFORMATION:

APPLICANT: Hoffmann-La Roche Inc.

TITLE OF INVENTION: thereof

TITLE OF INVENTION: thereof

TITLE OF INVENTION: thereof

TITLE OF INVENTION UNDER: 15094-07-08

CURRENT FILING DATE: 2004-07-08

PRIOR APPLICATION NUMBER: EP 03015526

PRIOR APPLICATION NUMBER: EP 03015526

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.2
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APPLICANT: LARRICK, JAMES W.
APPLICANT: MYCOFF, KEITH L.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY
TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES
CURRENT APPLICATION NUMBER: US/10/493,909
CURRENT FILING DATE: 2004-04-26
FRIOR APPLICATION NUMBER: 60/200,298
FRIOR PELING DATE: 2000-04-28
FRIOR PERING DATE: 2000-04-28
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                                                   140 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 199
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121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                       200 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 251
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219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
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APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: PC POLVPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022, 289
CURRENT APPLICATION NUMBER: US 60/531,752
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 11
LENGTH: 330
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Publication No. US20050260716A1
GENERAL INFORMATION:
APPLICANT: MOOIE, MAIGARE D.
TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
FILE REPERENCE: 02-16
CURRENT FILING DATE: 2005-03-08
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1.0
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Pred. No. 2.6e-101;
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97.0%; Pred. No. 2...
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Best Local Similarity 97.0
Matches 225; Conservative
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Best Local Similarity 97.0°
Matches 225; Conservative
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US-11-075-351-1
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; Sequence 68, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; TITLE OF INNEWITION: Angiopoietin-2 Specific Binding Agents
; TITLE OF INNEWITION UNMBER: US/10/982,440
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR PILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 68
                                                                                                       Query Match 97.2%; Score 1225; DB 6; Length 330; Best Local Similarity 97.0%; Pred. No. 2.6e-101; Matches 225; Conservative 3; Mismatches 4; Indels
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Pred. No. 2.6e-101;
3; Mismatches 4; Indels
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US-11-022-289-11
Sequence 11, Application US/11022289
Publication No. US2050249723A1
GENERAL INFORMATION:
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Best Local Similarity 97.0%;
Matches 225; Conservative
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-982-440-68
                                                             US-10-493-909-20
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Gaps

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APPLICANT: Protein Design Labs, Inc.
APPLICANT: Hinton, Paul R.
APPLICANT: Hinton, Paul R.
APPLICANT: Tso, J. Yun
APPLICANT: Tso, J. Yun
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: ANTHBODIES BY MUTAGENESIS
FILE OF INVENTION: ANTHBODIES BY MUTAGENESIS
FILE REPERENCE: 05882.0039.00PC03
CURRENT APPLICATION NUMBER: US/11/102,621
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                                                                                                           Length 330;
                                                                                                         Score 1225; DB 7;
Pred. No. 2.6e-101;
3; Mismatches 4;
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PRIOR APPLICATION NUMBER: US 10/822,300
PRIOR FILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Humanized antibody US-11-102-621-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 7, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
                                                                                                              97.2%;
                                                                                                                   Query Match
Best Local Similarity 97.0
Matches 225; Conservative
                   TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: artificial
                                                                  US-11-102-621-3
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Sequence 3, Application US/11102621

Publication No. US20050276799A1

GENERAL INFORMATION

APPLICANT: Hinton, Paul R.

APPLICANT: Tructubitta, Naoya

APPLICANT: Tructubitta, Naoya

APPLICANT: Tso, J. Yun

APPLICANT: Vasquez, Maximiliano

TITLE OF INVENTION: ALTERATION OF FCRN BINDING AFFINITIES OR SERUM HALF-LIVES OF

TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS

FILE REPERENCE: 058082.0039.00PC03

CURRENT APPLICATION NUMBER: US/11/102,621

CURRENT PILING DATE: 2005-04-08

PRIOR PILING DATE: 2004-04-09

PRIOR FILING DATE: 2004-04-09
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                                                                                                                                                                                                      APPLICANT: Presnell, Scott R.
APPLICANT: Novak. Wenfeng
APPLICANT: Novak. Juliae
APPLICANT: Novak. Juliae
APPLICANT: Novak. Juliae
APPLICANT: Whotmore, Theodore E.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE REFERENCE: 00-108
CURRENT APPLICATION NUMBER: US/11/165,141
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-10-207
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PageSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 330
                                                                                                                     S-11-165-141-15
Sequence 15. Application US/11165141
Publication No. US20050266485A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
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US-11-165-141-15
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Sequence 1, Application US/11233683
Sequence 1, Application US/11233683
Publication No. US20060025573A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
TITLE REFERENCE: LEX-017
CURRENT APPLICATION NUMBER: US/11/233,683
PRIOR PILING DATE: 2005-09-23
PRIOR PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
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; OTHER INFORMATION: human Ig gamma heavy chain C region
US-11-233-683-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.2%; Score 1225; DB 7; Best Local Similarity 97.0%; Pred. No. 2.6e-101; Matches 225; Conservative 3; Mismatches 4;
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97.0%; Pred. No. 2.6e-101;
tive 3; Mismatches 4;
PRIOR APPLICATION NUMBER: US 60/626,991
PRIOR FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/627,774
PRIOR PILING DATE: 2004-11-12
PRIOR FILING DATE: 2004-03-26
PRIOR FILING DATE: 2004-05-26
PRIOR FILING DATE: 2003-09-26
PRIOR FILING DATE: 2003-09-36
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR PILING DATE: 2003-09-36
NUMBER OF SEQ ID NOS: 11
SOGTWARE: PATENTIN VERSION 3.3
SOFTWARE: PATENTIN VERSION 3.3
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Best Local Similarity 97.04
Matches 225; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                       APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REPERBNCE: MER-131
CURRENT APPLICATION NUMBER: 10/495,146
PRIOR PILING DATE: 2004-05-10
PRIOR PILING DATE: 2004-05-10
PRIOR PILING DATE: 2004-05-11
PRIOR PILING DATE: 2001-111
PRIOR FILING DATE: 2001-11-12
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PRACESQ for Windows Version 4.0
IENGTH: 330
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APPLICANT: Dang, Wei
APPLICANT: Dasjarlais, John R.
APPLICANT: Marki, Sher Bahadur
APPLICANT: Vafa, Omid
APPLICANT: Hayes, Robert
TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILLE REFERENCE: A-71386-9
CURRENT APPLICATION NUMBER: US/11/124,620
CURRENT APPLICATION NUMBER: US 60/568,440
PRIOR APPLICATION NUMBER: US 60/569,906
PRIOR PILING DATE: 2004-07-15
PRIOR FILING DATE: 2004-07-20
                                                                                       Sequence 164, Application US/11005726
Publication No. US20060018903A1
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Publication No. US20060024298A1
GENERAL INFORMATION:
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                                                                                                                                             GENERAL INFORMATION:
APPLICANT: HELLENDOORN, Koen
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US-11-124-620-1
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Sequence 35, Application US/11024251

Publication No. US20050266425A1

GENERAL INFORMATION

APPLICANT: Zauderer, Maurice

APPLICANT: Paris, Mark

TITLE OF INVENTION Methods for Producing and Identifying Multispecific Antibodies

TITLE PEPERBUCE: 1843.0230001

CURRENT APPLICATION NUMBER: US/11/024,251

CURRENT APPLICATION NUMBER: 60/533,241

PRIOR FILING DATE: 2003-12-31

NUMBER OF SEQ ID NOS: 129

SOFTWARE: PatentIn version 3.3

SEQ ID NO 35

LENGTH: 335
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164 NWYVDGVEVHNAKTKPREEQ?NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALFAPIEKT 223
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97.2%; Score 1225; DB 7;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4;
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ORGANISM: Artificial
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US-11-024-251-35
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US-11-024-251-35
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February 22, 2006, 21:24:11; Search time 152.263 Seconds (without alignments) 669.475 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ABJ38647 ADA89055 ADD25647 ADG74307 ADX21627	AAE26274 ABB81490 AAE35214 AAY24154 AAE26273 ADJ52120	AEA89551 AAB47590 AEA891806 AAR91806 ADP56389 ADS82579 AAB47856 AAE21960 ABB81641	ALIGNMENTS 232 AA.
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235 235 235 235 235	247 251 251 267 269	2887 2887 2887 3320 3300 3300	protein;
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chain; Human; IgG1; immunoglobulin G; immunotherapy; immune disease; Fcepsilon receptor; autoimmune disease; constant region; heavy antialthamtic; antiallerapic; antiinflammatory; dermatological; antiathritic; antifreumatic; antidabetic; neuroprotective; Human IgG1 heavy chain constant region hinge-CH2-CH3 portion (first entry) hinge-CH2-CH3 region 28-MAR-2003

AA019665;

Homo sapiens.

WO200288317-A2.

07-NOV-2002.

01-MAY-2002; 2002WO-US013527

01-MAY-2001; 2001US-00847208. 24-OCT-2001; 2001US-00000439.

(REGC) UNIV CALIFORNIA.

ä Zhu Zhang K, Saxon A,

WPI; 2003-103456/09.

New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 19; Fig 3; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypoptide sequence capable of specific binding to a native Igd inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypoptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FeepsilonR). Also provided are nucleotide sequences encoding such a

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                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated bypersensitivity reaction, such as asthma, allergic thinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgGI heavy chain constant region hinge-CH2-CH3 portion
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                                                                                                                                                                                                                                                                                                                                                                            61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                             ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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Fcepsilon receptor; autoimmune disease; constant region; heavy chain;
antiasthmatic; antiallergic; antiinflammatory; dermatological;
antiarthritic; antirheumatic; antidiabetic; neuroprotective.
                                                                                                                                                                                                                                                                            1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                           Length 232;
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100.0%; Pred. No. 3.3e-91;
ive 0; Mismatches 0;
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24-OCT-2001; 2001US-00000439.
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232; Conservative
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present invention relates to a fusion molecule comprising a first

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              inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a mative IGE receptor (FoepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IGE-mediated biological response, preferably an IGE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angloedema or anaphylactic shock; or autoimmune diseases such as rhemmatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunicherapy. The present sequence is the human IgGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 NWYYDGVEVHNYKTKPREEQYNSTYRVVSVITVLHQNWMNGKEYKCKVSNKALPAPIEKT
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GE2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
polypeptide sequence capable of specific binding to a native IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; IgE; immunoglobulin E; immunotherapy; immune disease; Pcepsilon receptor; autoimmune disease; constant region; heavy antiallergic; antiinflammatory; dermatological; antiarthritic; antirheumatic; antitheumatic; neuroprotective;
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                                                                                                                                                                                                                                                                                                                 Length 330;
                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 1260; DB 6;
100.0%; Pred. No. 5.1e-91;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO19668 standard; protein; 569
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24-OCT-2001; 2001US-00000439.
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                                                                                                                                                                                                                                                   heavy chain constant region
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-103456/09
                                                                                                                                                                                                                                                                                    Sequence 330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion protein.
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conjypeptide sequence capable of specific binding to a native Igg inhibitory acceptor consisting of an immune receptor tyrosine-based inhibitory acceptor consisting of an immune receptor tyrosine-based inhibitory mutif (ITIM), expressed on mast cells, basophila or B cells, enctionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FeepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermattis, severe food allergies, chronic uriticaria, angiodedma or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of or symptoms resulting from, a type I hypersensitivity reaction in a conject receiving immunotherapy. The present sequence is a gammahinge-CHGamma2-(CHGamma2-(CHepsilon2-CHepsilon3-CHepsilon3-CHepsilon3 fusion protein (designated GE2) of the invention
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New fusion molecules comprising polypeptide sequences that bind to Ig inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autorimmune diseases.
                                                                                                                                            The present invention relates to a fusion molecule comprising a first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1260; DB 6; Best Local Similarity 100.0%; Pred. No. 9.7e-91; Matches 232; Conservative 0; Mismatches 0;
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                                                                                                     Claim 35; Fig 7; 116pp; English
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2003US-0519822P.
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12-NOV-2003;
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                                                                                                                                                                                        This invention relates to a novel MUC1 chimeric protein which comprises a first polypeptide sequence and a second polypeptide sequence, where the first polypeptide sequence is a MUC1 extracellular (MUC1-EC) polypeptide, and the second polypeptide sequence is a human immunoglobulin FC polypeptide or a human albumin polypeptide. The invention may be useful for the development of compounds with a cytostatic activity acting as MUC1 antagonists or CD27 antagonists. The MUC1 chimeric protein is useful in preparing a composition for treating cancer. The present sequence is that of a protein which was used during the development of the novel MUC1 chimeric protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region; antibody engineering; protein engineering;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin; mutein; fusion protein; cancer; cytostatic; neoplasm; autoimmune disease; immunosuppressive; immune disorder.
                                                                                             MUC1 ligand trap comprising a MUC1 extracellular polypeptide and an immunoglobulin FC polypeptide or an albumin polypeptide, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVLDSVGSFFLYSKLTVDKSRRQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 232;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 1232; DB 9;
Pred. No. 5.4e-89;
                                                                                                                                                                                                                                                                                                                                                                                                     97.8%; Score ... 5.4e-v
97.4%; Pred. No. 5.4e-v
                                                                                                                                                            Disclosure; SEQ ID NO 33; 82pp; English
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Matches 226; Conservative
                 Kufe DW;
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                                            WPI; 2005-346855/35.
                                                                                                                               treating cancer.
                                                               N-PSDB; ADZ87507
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 232 AA;
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               Kharbanda S,
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the invertion tradece to a mountained religions delected from cesidues 250, 314, and 428 (Kabat numbering) is different from that residues 250, 314, and 428 (Kabat numbering) is different from that comprising an PC residon protein. Also included are an FC fusion protein an actually identical to that of the courring class IgG antibody, a modified FC-fusion protein of the corresponding unmodified FC-fusion protein, a modified than that of the corresponding unmodified FC-fusion protein, a modified than that of the corresponding unmodified FC-fusion protein, a modified to residues 250, 314, and 428 is different from the group consisting of residues 250, 314, and 428 is different from the group consisting of residues 250, 314, and 428 is different from the group consisting of residues 260, 314, an isolated polynucleotide in the unmodified IgG class antibody), an isolated polynucleotide inclacule encoding a polypeptide comprising an esquence at least 90% identical to a sequence selected from ADZ656600-ADZ66556, an isolated comprising at least one amino acid sequence at least 90% identical to a sequence selected from ADZ656600-ADZ66556, an isolated comprising at least one amino acid sequence at least 90% identical to a sequence selected from ADZ656600-ADZ66556, an amino acid sequence at least one amino acid sequence at least from Comprising at least one amino acid residue as cited above, and comprising at least one amino acid residue as cited above, and different from chart present in the FC-fusion protein) and a method of producing a modified FC-fusion protein with an altered binding affinity for protein from protein comprising an enthal and a methor of producing a mitable protein from protein from protein with the unmodified FC-fusion protein an experient comprising an enthal and an enthal and a methor of producing a mitable protein from protein from protein comprising an enthal an altered and enthal and an enthal and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein (comprising preparing an expression vector comprising a suitable promoter operably linked to DNA encoding at least a constant region of an IgG heavy chain, transforming host cells with the vector and culturing the transformed host cells to produce the modified IgG Fc fusion protein). The modified antibody has a higher affinity for FcRn at pH 6.0 than at pH 8.0. The fusion proteins are useful for studying protein agents. The present sequence represents a human IgG1 heavy chain constant region with an amino acid substitution at residue 250, 314 or 428 (Rabat mumbering, the actual residue that is mutated is covered in the feature
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                                                                                                                                                                                                                                    New modified Fc-fusion protein where at least one amino acid residue from the heavy chain constant region, useful for studying protein function in vitro and in vivo and as potential therapeutic and diagnostic agents.
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Pred. No. 1.7e-88;
2; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                     Claim 21; SEQ ID NO 29; 170pp; English.
                                                                              (PROT-) PROTEIN DESIGN LABS INC.
15-OCT-2003; 2003US-0511687P.
14-APR-2004; 2004US-0562627P.
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97.4%;
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Best Local Similarity 97.4
Matches 226; Conservative
                                                                                                                                    Teurushita N;
                                                                                                                                                                                       WPI; 2005-315683/32
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                                                                                                                                    Hinton PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
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A novel recombinant vector has been developed which comprises a nucleotide sequence encoding a fusion protein. The fusion protein comprises three domains joined together in order, from N-terminus to C-terminus, of a first domain comprising a protein of interest, a second domain comprising a hydrophilic spacer and an affinity domain, each domain comprising amino acid residues. The present sequence represents the hinge/For region of human IgG1, used in example 3 of the present invention. The recombinant vector is used for the production of authentic recombinant proteins of interest. The method of the invention is useful for the expression of fusion proteins capable of isolation by affinity chromatography in pro- or eukaryotic cells. This method allows for the efficient cleavage and generation of authentic proteins of interest that do not contain extraneous (i.e. non-naturally occurring) amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant protein expression system for fusion protein production - useful for high quantity production of authentic recombinant proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ISKAKVORREPOVYTLPPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTP
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                                                                                                                                         Fusion protein; hydrophilic spacer; recombinant; expression system; carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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97.0%; Pred. No. 1.9e-88;
tive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 133-134; 194pp; English.
                 AAW26232 standard; protein; 232
                                                                                                                                                                                                                                                                                               97WO-US001470.
                                                                                                                                                                                                                                                                                                                                  96US-00595043.
                                                                                                                Human IgG1 hinge/Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                 (TECH-) TECHNOLOGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-402624/37.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT80158
                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                 WO9728272-A1
                                                                                                                                                                                                                                                                                                 31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                31-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                  Sgarlato GD;
                                                                                                                                                                                                                                                                  07-AUG-1997.
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PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232

181 279

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RESULT 7

(first entry)

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Preventing or treating lytic bone diseases, particularly associated w. cancer or metastasis, by administering an osteoprotegrin polypeptide.
                                                                                                                                                                                         Human; IgGgammal; anticancer; Antimetastatic; Osteogenic; lytic bone disease; multiple myeloma; immunoglobulin; osteosclerotic bone metastasis; OBG; osteoprotegrin; osteoclast formation inhibition; bone resorption inhibition.
                                                                                                                                                  Human IgGgammal hinge, CH2 and CH3 regions.
                        AAB80897 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             18-AUG-2000; 2000WO-US022806.
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                                                                                                                                                                                                                                                                                                                                          WO200117543-A2
                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-1999;
                                                                                                           31-MAY-2001
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                                                                   AAB80897;
    AAB80897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence was used in the production of AGP-1 fusion proteins. AGP-1 is a type II transmembrane protein. The fusion proteins comprise an Pc immunoglobulin region fused to the N-terminal portion of the AGP-1 and protein. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-breast, prosites. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1 proteins used in prior art therapies
                                                                                                                                                                 Human; AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
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                                                                                                                            Human IgGgammal hinge, CH2 and CH3 regions.
AAB28690 standard; protein; 232
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                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 232 AA;
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                                                                                                                                                                                                                                                                                                                                                         WO200063253-A1.
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                                                                                   14-FEB-2001
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                                                                                                                                                                                                                                                                          IgGgammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hen H,
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99US-00389545

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                                                                                      of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-AAB80905) can inhibit formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The present sequence is the hings. CH2 and CH3 regions of human IgGgammal. This sequence can be used to generate fusion proteins of OPG and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for the prevention or treatment
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                                                                                                                                                                                                                                                                                                                                                 immunoglobulin, for use in the present invention. The generated fusion proteins can exhibit increased circulating half-lives and slower clearance times, thereby providing a more sustained activity
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97.0%; Pred. No. 1.9e-88;
iive 3; Mismatches 4;
Disclosure, Fig 1; 87pp; English.
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RESULT 9

RESULT

PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232

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ð 유 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180

(first entry)

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AAE15347 standard; protein; 232 AA.
                                                                09-APR-2002
                                 AAE15347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses fusion protein comprising human osteoprotegerin (OPG) protein fused by linker to human 1gG1 Pc portion. OPG negatively regulates formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPG-Pc fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hyperalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic loosening. The present sequence is partial human immunoglobulin G (Ig G) in protein comprising the hinge and heavy chain constant regions CH2 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.
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                                                                                                   Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.
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Pred. No. 1.9e-88;
3; Mismatches 4
      standard, protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mann MB
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97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-244572/25.
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                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 232 AA;
                                                                                                                                                                                                                                                                  WO200118203-A1.
                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1999;
                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Simi
Matches 225;
                                                                      13-JUN-2001
                                                                                                                                                                                                                                                                                                  15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                      AAY72915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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        AAY72915
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The invention relates to a method for increasing and maintaining
chaematocrit in a mammal. The method comprises administering a
chaematocrit in a mammal. The method comprises administering a
composition, less frequently than an equivalent molar amount of and at a
composition, less frequently than an equivalent molar amount of and at a
comparable target haematocrit. Epo is a glycoptotein hormone necessary
comparable target haematocrit. Epo is a glycoptotein hormone necessary
comparable target haematocrit in a mammal suffering from anaemia
associated with a decline or loss of kidney function, myelosuppressive
therapy comprising chemotherapeutic or anti-viral drugs or associated
with excessive blood loss during surgical procedures, and in cancer
condition. The present sequence is human immunoglobulin G (1gG) gamma 1
constant heavy chain (CH2, CH3) hinge region used to construct Epo
hyperglycosylated analogue fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increasing and maintaining hematocrit in mammal suffering from anemia, comprising administering hyperglycosylated analog of erythropoietin less frequently and at lower molar amount of recombinant human erythropoietin.
                                                       Human; erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG; cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.
Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKKKDTLMISKTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.2%; Score 1225; DB 5;
97.0%; Pred. No. 1.9e-88;
iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sitney KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Browne JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 10; 95pp; English
                                                                                                                                                                                                                                                                                                                                    19-APR-2001; 2001WO-US012836.
                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000; 2000US-00559001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elliott SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-034433/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 232 AA;
                                                                                                                                                                                                                   WO200181405-A2.
                                                                                                                                                            Ното варіелв.
                                                                                                                                                                                                                                                                          01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Egrie JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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RESULT 11

1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF

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The invention relates to a compound comprising an immunoglobulin (Ig)
heavy chain constant region or its fragment that retains the ability to
bind an Fo receptor linked by a linker group or a direct bond to a
c peptide capable of binding an amyloidogenic protein. The invention is
c useful for clearing an amyloidogenic protein The invention is
c useful for clearing an amyloidogenic protein The invention is
c transthyretin (TTR), prion protein (PPP), islet amyloid, polypeptide
(TAPP), atrial natriuretic factor (AMP), kappa light chain, lambda light
(TAPP), atrial natriuretic factor (AMP), kappa light chain, lambda light
c (TAPP), atrial natriuretic factor (AMP), kappa light chain, lambda light
c (TAPP), atrial natriuretic factor (AMP), kappa light chain, lambda light
c chain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I,
c gelsolin, calcitonin, fibrinogen, Huntington, alpha-synocher such
as Alzheimer & disease and spongiform encephalopathy. Disorders treatable
as Alzheimer, disease and spongiform encephalopathy in cows and
c lysolated those caused or characterised by deposits of TTR (eg. familial
amyloid cardiomyopathy), PPP (eg. spongiform encephalopathy in cows and
c creutzfeldt-Jacob disease (CJ) and Gerstmann-Straussler-Scheinker
syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),
C (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg.
c diopathic amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal
amyloidosis), Lysozyme (eg. hereditary systemic amyloidosis). Other
examples of amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal
amyloidosis), Lysozyme (eg. hereditary systemic amyloidosis).
C used in the exemplification of the invention
                                                                                                                                                                                                    Human, amyloidogenic protein, Alzheimer's disease, Huntington's disease, spongiform encephalopathy, familial amyloid cardiomyopathy; amyloidosis, Gerstmann-Straussler-Scheinker syndrome; spongiform encephalopathy, GSS; Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel therapeutic agent useful for treating an amyloidogenic disorder, e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain constant region linked to a peptide capable of binding amyloidogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.2%; Score 1225; DB 5; Length 232; 97.0%; Pred. No. 1.9e-88; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gosselin M;
                   AAE26272 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 8; Page 76; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Israel DI, Joyal JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-NOV-2001; 2001WO-US044581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-2000; 2000US-0253302P.
29-NOV-2000; 2000US-0250198P.
20-DEC-2000; 2000US-0257186P.
                                                                                                            14-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PRAE-) PRAECIS PHARM INC.
                                                                                                                                                          Human IgGl heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-636427/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 AA;
                                                                                                                                                                                                                                                                                                                                                                                              WO200242462-A2.
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gefter ML,
                                                                 AAE26272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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AAE26272
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                                                                                        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the
61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises a therapeutic agent for treating endotoxin induced disease, the therapeutic agent contains a fusion protein of the Herpes virus entry mediator (HVEM) protein and an immunoglobulin Fc domain. The therapeutic agent of the invention is useful for treating endotoxin induced disease, such as endotoxic shock. The present amino acid sequence represents a human protein which is claimed in the
                                 61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                     ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKBYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New therapeutic agent, useful for treating endotoxin induced disease, comprises fusion protein of Herpes virus entry mediator protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                      181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                      PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                               therapeutic agent, endotoxin induced disease, fusion protein, Herpes virus entry mediator, HVEM; immunoglobulin Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.2%; Score 1225; DB 7; Best Local Similarity 97.0%; Pred. No. 1.9e-88; Matches 225; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                               Herpes virus entry mediator-related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; SEQ ID NO 2; 11pp; Japanese.
                                                                                                                                                                                                                                                          Ŕ
                                                                                                                                                                                                                                                        ADJ65991 standard; protein; 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2001; 2001JP-00328430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2001; 2001JP-00328430
                                                                                                                                                                                                                                                                                                                             06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TAIS ) TAISHO PHARM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENE TECHNO SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                 endotoxic shock; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-817833/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADJ65998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP2003128576-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                     121
                                                                                                                                                                                                                                                                                           ADJ65991;
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                                                                                                                                                                                                                                          ADJ6599
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Conservative

Local Similarity Les 225; Conserv

Best Loca Matches

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Gaps

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The invention relates to a compound (I) binding to tissue factor (TF).

The compound (I) has the formula A-(LM)-C, where A is a FVIIa polypeptide, LM is an optional linker group, C comprises an optional linker group, C comprises an optional linker group, C comprises an endiated activated factor domain, and (I) binds to TF. (I) inhibits TF-medicament, and for the manufacture of a medicament for preventing or treating disease or disorder associated with pathophysiological TF activity. The disease or disorder associated with pathophysiological TF activity are deep venous thrombosis, arterial thrombosis, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transdermal coronary angioplastry (PTGA), stroke, cancer, tumor metastasis, angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis, angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis, andiogenesis, ischemia/reperfusion, septic shock, septic andiogenesis and restenoses following angioplastry, acute and chronic indications such as inflammation, septic shock, septicemia, hypotension, adult respiratory distress syndrome (ARDS), disseminated intravascular cadult respiratory distress syndrome (ARDS), disseminated intravascular cagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial infarction, or prophylactic treatment of mammals with atherosclerotic vessels at risk for thrombosis. The present sequence represente the Fc domain fragment of human immunoglobulin GI (1961).
ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                            TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic; cerebroprotective; cytostatic; vasotropic; antihumanic; antihumaniarhritic; antitateriosclerotic; antiinlammatory; antibacterial; immunosuppressive; hypertensive; cardiant; coagulation Factor VII; human; immunoglobulin G1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating diseases such
                         ISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                    PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 232;
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97.0%; Pred. No. 1.9e-88;
iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compound binding to tissue factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as anglogenesis, ischemia/reperfusion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steenstrup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; SEQ ID NO 7; 61pp; English.
                                                                                                                                                                                                                                               ADJ57512 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                  Human IgG1 Fc domain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUL-2003; 2003WO-DK000481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUL-2002; 2002DK-00001099
                                                                                                                                                                                                                                                                                                                                     06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-180224/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                           ADJ57512;
                                                                                    181
                                       121
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1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Gaps

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4; Indels

Best Local Similarity 97.0 Matches 225; Conservative

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Similarity

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(HUEPD), a peptide linker, and a human IgG Fc variant, is new.

(HUEPD), a peptide linker, and a human IgG Fc variant, is new.

(HUEPD), a peptide linker, and a human IgG Fc variant, is new.

(INDEPRINENT CLAIMS are also included for the following: a chinese hamster ovary (CHO)-derived cell line producing the HUEPO-L-VFC fusion procein in its growth medium in excess of 10 kmicro;g per million cells in a 24 hour period; an entend for making a recombinant fusion protein comprising HUEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred protein: The peptide linker containing 20 or fewer amino acids is present between HUEPO and the human IgG Fc variant, alanine, and threonine. The human IgG Fc variant, serine, alanine, and threonine. The human IgG Fc variant, serine, serine, alanine, and threonine. The human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human IgG Vaith pro311Ser mutations comprising 417 amino acids (SEQ ID NO. 18).

20). It further comprises a hinge, CH2, and CH3 domains of human IgG L with Leu234Val, Leu235Ala mutations comprising 437 amino acids (SEQ ID NO. 22). The HUEPO-L-VFC fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or rheumatoid arthritis.
                                                                           ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antianaemic; nephrotropic; human; HuBPO-L-vFc; erythropoietin; EPO; anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis; AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAP1EKT
                                                                                                                                                                                                                           PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 26; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 1gG1 hinge and CH2 region.
                                                                                                                                                                                                                                                                                                                                     ADR48992 standard; peptide; 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-2004; 2004US-00761593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-2001; 2001US-00932812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sun CRY;
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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(SUNB/) SUN B N C.
(SUNC/) SUN C R Y.
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29-APR-2004; 2004WO-EP004562 30-APR-2003; 2003US-0467206P

WO2004096976-A2 11-NOV-2004. (NOVS) NOVARTIS AG. (NOVS) NOVARTIS PHARMA G! (SCRI) SCRIPPS RES INST.

Kaye J, Wilkinson B; WPI; 2004-804740/79.

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basis. Preferred CHO-Derived Cell Line:
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New purified spleen expressed (SPEX) polypeptide useful for modulating lymphocyte activation and the immune response in disorders including autoimmunity, cancer, transplant rejection and inflammation.

Disclosure; SEQ ID NO 97; 98pp; English.

Sequence 232 AA;

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                                                                                                                                                                                                                                    ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                            1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKF
                                                                                                                                                                                             61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                            Gaps
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Ouery Match 97.2%; Score 1225; DB 8; Length 232; Best Local Similarity 97.0%; Pred. No. 1.9e-88; Matches 225; Conservative 3; Mismatches 4; Indels (
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ADU51146 standard; protein; 232 AA.
                (first entry)
                27-JAN-2005
        ADU51146;
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Human spleen-expressed receptor-related solubility-promoting protein.

immunosuppressive; cytostatic; antiinflammatory; immune modulation; intercellular communication; autoimmune disease; cancer; neoplasm; transplant rejection; immune disorder; inflammation; gene therapy.

Homo sapiens

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121 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel purified polypeptide comprising any of SEQ ID NOS: 3, 7, 9, 11, 45 or 88, or an amino acid sequence that is 95% or more identical to the amino acid sequences and which includes an immunoglobulin like domain structure. The polypeptide of the invention activities and is a spleen-expressed (SERS) polypeptide. The methods and compositions of the present invention may useful for modulating lymphocyte activation and the immune response in a variety of conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            including autolumnunity, cancer, transplant rejection and inflammation. Such modulation may be achieved via the use of gene therapy. The current sequence is that of the human spleen expressed (SPEX) receptor-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     solubility-promoting protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 232 AA;
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